

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 15, 2005, 18:18:32 ; Search time 204 Seconds
(without alignments)
7275.015 Million cell updates/sec

Title: US-09-989-733-398

Perfect score: 907

Sequence: 1 ggcactctgaaggtcccaagc.....gtgagactccatccacaca 907

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database: Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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3	601.6	66.3	1154	US-09-799-451-704	Sequence 204, App
4	500	55.1	500	US-09-276-531-73	Sequence 73, Appl
5	211.8	23.4	160759	US-09-949-016-16514	Sequence 16514, A
6	211.8	23.3	23533	US-09-949-016-15377	Sequence 15377, A
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8	210.6	23.2	64813	US-09-949-016-11957	Sequence 11957, A
9	210.6	23.2	70131	US-09-949-016-16064	Sequence 16064, A
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19	209.2	23.1	59065	US-10-135-686-3	Sequence 3, Appl1
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145	205.2	22.6	601	4	US-09-949-016-149196	Sequence 149196, A
146	205.2	22.6	8345	4	US-09-949-016-16833	Sequence 16833, A
147	205.2	22.6	12013	4	US-09-949-016-15938	Sequence 15938, A
148	205.2	22.6	12013	4	US-09-949-016-15939	Sequence 15939, A
149	205.2	22.6	42373	4	US-09-949-016-16438	Sequence 16438, A
150	205.2	22.6	601	4	US-09-949-016-184743	Sequence 184743, A
151	204.8	22.6	601	4	US-09-949-016-148190	Sequence 148190, A
152	204.8	22.6	601	4	US-09-949-016-149192	Sequence 149192, A
153	204.8	22.6	601	4	US-09-949-016-149195	Sequence 149195, A
154	204.8	22.6	601	4	US-09-949-016-149197	Sequence 149197, A
155	204.8	22.6	74804	4	US-09-949-016-15118	Sequence 15118, A
156	204.6	22.6	601	4	US-09-949-016-33416	Sequence 33416, A
157	204.6	22.6	601	4	US-09-949-016-41051	Sequence 41051, A
158	204.6	22.6	42954	4	US-09-949-016-17123	Sequence 17123, A
159	204.6	22.6	42954	4	US-09-949-016-17124	Sequence 17124, A
160	204.6	22.6	66055	4	US-09-949-016-13292	Sequence 13292, A
161	204.6	22.6	88950	4	US-09-949-016-17150	Sequence 17150, A
162	204.4	22.5	10029	4	US-09-949-016-11846	Sequence 11846, A
163	204.4	22.5	10029	4	US-09-949-016-16140	Sequence 16140, A
164	204.4	22.5	104520	4	US-09-949-016-13503	Sequence 13503, A
165	204.4	22.5	126029	4	US-09-949-016-14731	Sequence 14731, A
166	204.4	22.5	144158	4	US-09-949-016-11755	Sequence 11755, A
167	204.4	22.5	144158	4	US-09-949-016-12936	Sequence 12936, A
168	204.4	22.5	363032	4	US-09-949-016-12415	Sequence 12415, A
169	204.4	22.5	363032	4	US-09-949-016-15754	Sequence 15754, A
170	204.2	22.5	4736	4	US-09-526-193A-15	Sequence 15, Appl
171	204.2	22.5	98864	4	US-09-949-016-15403	Sequence 15403, A
172	204	22.5	601	4	US-09-949-016-120817	Sequence 120817, A
173	204	22.5	7561	4	US-09-949-016-11816	Sequence 11816, A
174	204	22.5	7562	4	US-09-949-016-13895	Sequence 13895, A
175	204	22.5	28556	4	US-09-949-016-11064	Sequence 11064, A
176	204	22.5	40037	4	US-09-949-016-12715	Sequence 12715, A
177	204	22.5	43335	4	US-09-949-016-12909	Sequence 12909, A
178	204	22.5	189560	4	US-09-949-016-11202	Sequence 11202, A
179	204	22.5	421118	4	US-09-949-016-12927	Sequence 16297, A
180	203.8	22.5	99900	3	US-09-949-016-10	Sequence 10, Appl
181	203.8	22.5	601	4	US-09-949-016-13106	Sequence 163106, A
182	203.6	22.4	25122	4	US-09-949-016-16389	Sequence 16389, A
183	203.6	22.4	175265	4	US-09-949-016-16083	Sequence 14172, A
184	203.6	22.4	194393	4	US-09-949-016-14172	Sequence 33415, A
185	203.4	22.4	601	4	US-09-949-016-41050	Sequence 41050, A
186	203.4	22.4	30456	4	US-09-949-016-14213	Sequence 14213, A
187	203.4	22.4	44439	4	US-09-949-016-11202	Sequence 17202, A
188	203.4	22.4	44439	4	US-09-949-016-11904	Sequence 12904, A
189	203.4	22.4	47727	4	US-09-949-016-12539	Sequence 12539, A
190	203.4	22.4	62128	4	US-09-949-016-11292	Sequence 17292, A
191	203.4	22.4	112114	4	US-09-949-016-11894	Sequence 11894, A
192	203.4	22.4	154605	4	US-09-949-016-11715	Sequence 17175, A
193	203.4	22.4	22750	4	US-09-949-016-13597	Sequence 13597, A
194	203.2	22.4	98439	4	US-09-949-016-13597	Sequence 12596, A
195	203.2	22.4	136264	4	US-09-949-016-13061	Sequence 13061, A
196	203.2	22.4	136265	4	US-09-949-016-13061	Sequence 12733, A
197	203.2	22.4	178883	4	US-09-949-016-13039	Sequence 13039, A
198	203.2	22.4	178884	4	US-09-949-016-13418	Sequence 13418, A
199	203.2	22.4	236474	4	US-09-949-016-13417	Sequence 33417, A
200	203	22.4	601	4	US-09-949-016-33418	Sequence 33418, A
201	203	22.4	601	4	US-09-949-016-33419	Sequence 33419, A
202	203	22.4	601	4	US-09-949-016-33419	Sequence 41052, A
203	203	22.4	601	4	US-09-949-016-41052	Sequence 41053, A
204	203	22.4	601	4	US-09-949-016-41053	Sequence 41054, A
205	203	22.4	601	4	US-09-949-016-41054	Sequence 11951, A
206	203	22.4	40742	4	US-09-949-016-11751	Sequence 13047, A
207	203	22.4	40747	4	US-09-949-016-11597	Sequence 13547, A
208	203	22.4	46085	4	US-09-949-016-13547	Sequence 13548, A
209	203	22.4	46085	4	US-09-949-016-13548	Sequence 15174, A
210	203	22.4	56441	4	US-09-949-016-15174	Sequence 15175, A
211	203	22.4	56441	4	US-09-949-016-15175	Sequence 15784, A
212	203	22.4	69709	4	US-09-949-016-15787	Sequence 15687, A
213	203	22.4	107458	4	US-09-949-016-16887	Sequence 3, Appl1
214	203	22.4	114793	4	US-10-148-806-3	Sequence 14302, A
215	203	22.4	123463	4	US-09-949-016-14202	Sequence 12449, A
216	203	22.4	146639	4	US-09-949-016-13449	Sequence 17504, A
217	203	22.4	276337	4	US-09-949-016-17504	Sequence 5, Appl1
218	202.8	22.4	27667	4	US-09-841-159-5	Sequence 13225, A
219	202.8	22.4	40168	4	US-09-949-016-11225	Sequence 16881, A
220	202.8	22.4	51508	4	US-09-949-016-16881	Sequence 15095, A
221	202.8	22.4	93510	4	US-09-949-016-15095	Sequence 23936, A
222	202.6	22.3	601	4	US-09-949-016-12396	Sequence 139600, A
223	202.6	22.3	601	4	US-09-949-016-18623	Sequence 16270, A
224	202.6	22.3	23832	4	US-09-949-016-16270	Sequence 13027, A
225	202.6	22.3	45198	4	US-09-949-016-13027	Sequence 13626, A
226	202.6	22.3	68392	4	US-09-949-016-12626	Sequence 12684, A
227	202.6	22.3	68392	4	US-09-949-016-12626	Sequence 17449, A
228	202.6	22.3	69763	4	US-09-949-016-15784	Sequence 191425, A
229	202.4	22.3	601	4	US-09-949-016-131425	Sequence 17222, A
230	202.4	22.3	26007	4	US-09-949-016-11222	Sequence 16960, A
231	202.4	22.3	31713	4	US-09-949-016-15960	Sequence 13101, A
232	202.4	22.3	44447	4	US-09-949-016-11018	Sequence 12101, A
233	202.4	22.3	44447	4	US-09-949-016-11101	Sequence 16188, A
234	202.4	22.3	62354	4	US-09-949-016-11878	Sequence 12270, A
235	202.4	22.3	62354	4	US-09-949-016-12270	Sequence 13525, A
236	202.4	22.3	109690	4	US-09-949-016-13525	Sequence 12938, A
237	202.4	22.3	115635	4	US-09-949-016-12396	Sequence 15316, A
238	202.4	22.3	144322	4	US-09-949-016-13316	Sequence 17590, A
239	202.4	22.3	247599	4	US-09-949-016-11590	Sequence 8, Appl1
240	202.2	22.3	9365	3	US-09-608-285A-8	Sequence 8, Appl1
241	202.2	22.3	9365	3	US-09-350-832B-8	Sequence 8, Appl1
242	202.2	22.3	9365	3	US-09-370-265-8	Sequence 8, Appl1
243	202.2	22.3	9365	3	US-09-557-800C-8	Sequence 8, Appl1
244	202.2	22.3	9365	3	US-09-557-800C-8	Sequence 8, Appl1
245	202.2	22.3	9365	3	US-09-370-622A-8	Sequence 42, Appl1
246	202.2	22.3	14747	3	US-09-608-285A-8	Sequence 42, Appl1

C 247	202.2	22.3	14747	4	US-09-557-800C-42	Sequence 42, Appl	320	201	22.2	108441	4	US-09-949-016-14090	Sequence 14090, A
C 248	202.2	22.3	15977	3	US-09-608-285A-59	Sequence 59, Appl	321	201	22.2	167708	4	US-09-949-016-14423	Sequence 16423, A
C 249	202.2	22.3	24593	4	US-09-949-016-13333	Sequence 13433, A	322	200.8	22.1	44221	2	US-08-257-965B-9	Sequence 9, Appl1
C 250	202.2	22.3	30843	4	US-09-949-016-14487	Sequence 14487, A	323	200.8	22.1	44221	3	US-08-367-841A-9	Sequence 9, Appl1
C 251	202.2	22.3	91831	4	US-09-949-016-13694	Sequence 13694, A	324	200.8	22.1	44221	5	US-08-520-373D-6	Sequence 6, Appl1
C 252	202.2	22.3	107897	4	US-09-949-016-13118	Sequence 13118, A	325	200.8	22.1	44221	5	PCR-US95-07201-9	Sequence 9, Appl1
C 253	202.2	22.3	107937	4	US-09-949-016-17192	Sequence 17192, A	326	200.8	22.1	11729	4	US-09-949-016-13247	Sequence 13247, A
C 254	202.2	22.3	116425	4	US-09-949-016-11809	Sequence 11809, A	327	200.8	22.1	11729	4	US-09-949-016-13123	Sequence 13123, A
C 255	202.2	22.3	116455	4	US-09-949-016-13675	Sequence 13675, A	328	200.8	22.1	13445	4	US-09-949-016-15152	Sequence 13512, A
C 256	202.2	22.3	235452	4	US-09-949-016-13414	Sequence 33414, A	329	200.8	22.1	95122	4	US-09-949-016-11235	Sequence 17255, A
C 257	202	22.3	601	4	US-09-949-016-41049	Sequence 41049, A	330	200.8	22.1	109328	4	US-09-949-016-16926	Sequence 16926, A
C 258	202	22.3	601	4	US-09-949-016-12926	Sequence 12026, A	331	200.8	22.1	107820	4	US-09-792-616-1	Sequence 1, Appl1
C 259	202	22.3	168104	4	US-09-949-016-16554	Sequence 16554, A	332	200.8	22.1	319608	4	US-09-539-333D-1	Sequence 1, Appl1
C 260	201.8	22.2	27783	4	US-09-949-016-16736	Sequence 16736, A	333	200.8	22.1	319608	4	US-09-949-016-16045	Sequence 16045, A
C 261	201.8	22.2	50518	4	US-09-949-016-12315	Sequence 12315, A	334	200.6	22.1	39601	4	US-09-813-133A-3	Sequence 3, Appl1
C 262	201.8	22.2	51111	4	US-09-949-016-12069	Sequence 12069, A	335	200.6	22.1	55827	3	US-10-212-877-3	Sequence 3, Appl1
C 263	201.8	22.2	51111	4	US-09-949-016-15724	Sequence 15724, A	336	200.6	22.1	55827	3	US-10-212-877-3	Sequence 3, Appl1
C 264	201.8	22.2	56551	4	US-09-949-016-12030	Sequence 12030, A	337	200.6	22.1	74804	4	US-09-949-016-15964	Sequence 15964, A
C 265	201.8	22.2	58782	4	US-09-949-016-16851	Sequence 16851, A	338	200.6	22.1	90618	4	US-09-949-016-15513	Sequence 12513, A
C 266	201.8	22.2	60417	4	US-09-949-016-13312	Sequence 13312, A	339	200.6	22.1	103887	4	US-09-949-016-17050	Sequence 17050, A
C 267	201.8	22.2	60572	4	US-09-949-016-12702	Sequence 12702, A	340	200.6	22.1	103887	4	US-09-949-016-17561	Sequence 17562, A
C 268	201.8	22.2	60592	4	US-09-949-016-13741	Sequence 13741, A	341	200.6	22.1	113379	4	US-09-949-016-15612	Sequence 15610, A
C 269	201.8	22.2	84763	4	US-09-949-016-11919	Sequence 11919, A	342	200.6	22.1	113379	4	US-09-949-016-15640	Sequence 15640, A
C 270	201.8	22.2	84763	4	US-09-949-016-13914	Sequence 13914, A	343	200.4	22.1	13985	4	US-09-949-016-15602	Sequence 15602, A
C 271	201.8	22.2	131332	4	US-09-949-016-15335	Sequence 15335, A	344	200.4	22.1	13985	4	US-09-949-016-15640	Sequence 15640, A
C 272	201.8	22.2	131332	4	US-09-949-016-15335	Sequence 15335, A	345	200.4	22.1	13985	4	US-09-949-016-15608	Sequence 15608, A
C 273	201.8	22.2	234288	4	US-09-949-016-17272	Sequence 17272, A	346	200.4	22.1	13985	4	US-09-949-016-15608	Sequence 15608, A
C 274	201.8	22.2	285986	4	US-09-949-016-12887	Sequence 12887, A	347	200.4	22.1	13985	4	US-09-949-016-17188	Sequence 17188, A
C 275	201.8	22.2	288031	4	US-09-949-016-14864	Sequence 14864, A	348	200.4	22.1	13985	4	US-09-949-016-18864	Sequence 18864, A
C 276	201.6	22.2	288031	4	US-09-949-016-15683	Sequence 15683, A	349	200.4	22.1	13985	4	US-09-949-016-18864	Sequence 18864, A
C 277	201.6	22.2	29614	4	US-09-949-016-12590	Sequence 12590, A	350	200.4	22.1	52824	4	US-09-949-016-15857	Sequence 15857, A
C 278	201.6	22.2	46319	4	US-09-949-016-12526	Sequence 12526, A	351	200.4	22.1	52824	4	US-09-949-016-15857	Sequence 15857, A
C 279	201.6	22.2	46319	4	US-09-949-016-12526	Sequence 12526, A	352	200.4	22.1	103887	4	US-09-949-016-12513	Sequence 12513, A
C 280	201.6	22.2	50959	4	US-09-949-016-16659	Sequence 16659, A	353	200.4	22.1	103887	4	US-09-949-016-17050	Sequence 17050, A
C 281	201.6	22.2	246240	2	US-08-724-394A-20	Sequence 20, Appl	354	200.2	22.1	601	4	US-09-949-016-12083	Sequence 12083, A
C 282	201.6	22.2	246240	2	US-08-724-394A-21	Sequence 21, Appl	355	200.2	22.1	601	4	US-09-949-016-12116	Sequence 12116, A
C 283	201.6	22.2	246240	2	US-08-724-394A-22	Sequence 22, Appl	356	200.2	22.1	601	4	US-09-949-016-127564	Sequence 127564, A
C 284	201.4	22.2	601	4	US-09-949-016-40426	Sequence 40426, A	357	200.2	22.1	601	4	US-09-949-016-16708	Sequence 16708, A
C 285	201.4	22.2	601	4	US-09-949-016-16981	Sequence 16981, A	358	200.2	22.1	601	4	US-09-949-016-169914	Sequence 169914, A
C 286	201.4	22.2	601	4	US-09-949-016-181571	Sequence 181571, A	359	200.2	22.1	601	4	US-09-949-016-185499	Sequence 185499, A
C 287	201.4	22.2	601	4	US-09-949-016-181572	Sequence 181572, A	360	200.2	22.1	10615	4	US-09-949-016-13136	Sequence 13136, A
C 288	201.4	22.2	15720	4	US-09-949-016-11780	Sequence 11780, A	361	200.2	22.1	10615	4	US-09-949-016-13465	Sequence 13465, A
C 289	201.4	22.2	15739	4	US-09-949-016-14233	Sequence 14233, A	362	200.2	22.1	28257	4	US-09-949-016-13076	Sequence 13076, A
C 290	201.4	22.2	29165	4	US-09-949-016-12340	Sequence 12340, A	363	200.2	22.1	28257	4	US-09-949-016-15315	Sequence 15315, A
C 291	201.4	22.2	29771	4	US-09-949-016-12754	Sequence 12754, A	364	200.2	22.1	61313	4	US-09-949-016-15338	Sequence 15338, A
C 292	201.4	22.2	29771	4	US-09-949-016-13956	Sequence 13956, A	365	200.2	22.1	61313	4	US-09-949-016-11772	Sequence 11772, A
C 293	201.4	22.2	29771	4	US-09-949-016-12032	Sequence 12032, A	366	200.2	22.1	71574	4	US-09-949-016-15880	Sequence 15880, A
C 294	201.4	22.2	40655	4	US-09-949-016-15919	Sequence 15919, A	367	200.2	22.1	83349	4	US-09-949-016-17149	Sequence 17149, A
C 295	201.4	22.2	40655	4	US-09-949-016-15919	Sequence 15919, A	368	200.2	22.1	106746	4	US-09-326-402C-1	Sequence 1, Appl1
C 296	201.4	22.2	58593	4	US-09-949-016-12232	Sequence 12232, A	369	200.2	22.1	106746	4	US-09-326-402C-12	Sequence 12, Appl
C 297	201.4	22.2	64467	4	US-09-803-671B-3	Sequence 3, Appl1	370	200.2	22.1	114139	4	US-09-949-016-16836	Sequence 16836, A
C 298	201.4	22.2	64467	4	US-10-274-409-3	Sequence 3, Appl1	371	200.2	22.1	114139	4	US-09-949-016-13413	Sequence 13413, A
C 299	201.4	22.2	68529	4	US-09-949-016-12140	Sequence 12140, A	372	200.2	22.1	114139	4	US-09-949-016-16264	Sequence 16264, A
C 300	201.2	22.2	68529	4	US-09-949-016-15357	Sequence 15357, A	373	200.2	22.1	240157	4	US-09-949-016-24898	Sequence 24898, A
C 301	201.2	22.2	68529	4	US-09-949-016-15357	Sequence 15357, A	374	200.2	22.1	240157	4	US-09-949-016-24898	Sequence 24898, A
C 302	201.2	22.2	68529	4	US-09-949-016-15671	Sequence 15671, A	375	200.2	22.1	601	4	US-09-949-016-33413	Sequence 33413, A
C 303	201.2	22.2	79835	4	US-09-949-016-12456	Sequence 12456, A	376	200.2	22.1	601	4	US-09-949-016-41048	Sequence 41048, A
C 304	201.2	22.2	79835	4	US-09-949-016-16121	Sequence 16121, A	377	200.2	22.1	601	4	US-09-949-016-138409	Sequence 138409, A
C 305	201.2	22.2	79835	4	US-09-949-016-13032	Sequence 13032, A	378	200.2	22.1	601	4	US-09-949-016-200753	Sequence 200753, A
C 306	201.2	22.2	165651	4	US-09-949-016-12882	Sequence 12882, A	379	200.2	22.1	601	4	US-09-949-016-200754	Sequence 200754, A
C 307	201.2	22.2	256176	4	US-09-949-016-15524	Sequence 15524, A	380	200.2	22.1	601	4	US-09-949-016-200899	Sequence 200899, A
C 308	201	22.2	256176	4	US-09-949-016-127563	Sequence 127563, A	381	200	22.1	601	4	US-09-949-016-200900	Sequence 200900, A
C 309	201	22.2	601	4	US-09-949-016-169369	Sequence 169369, A	382	200	22.1	601	4	US-09-949-001-480	Sequence 48, Appl
C 310	201	22.2	601	4	US-09-949-016-170444	Sequence 170444, A	383	200	22.1	601	4	US-09-949-001-880	Sequence 800, Appl
C 311	201	22.2	601	4	US-09-949-016-178914	Sequence 178914, A	384	200	22.1	22334	4	US-09-949-016-13377	Sequence 13377, A
C 312	201	22.2	8180	4	US-09-949-016-14472	Sequence 14472, A	385	200	22.1	41863	4	US-09-949-016-14948	Sequence 14948, A
C 313	201	22.2	9779	4	US-09-949-016-15370	Sequence 15370, A	386	200	22.1	44430	4	US-09-949-016-15882	Sequence 15882, A
C 314	201	22.2	14160	4	US-09-949-016-16894	Sequence 16894, A	387	200	22.1	44430	4	US-09-949-016-15882	Sequence 15882, A
C 315	201	22.2	34011	4	US-09-949-016-12485	Sequence 12485, A	388	200	22.1	46816	4	US-09-949-016-13493	Sequence 13493, A
C 316	201	22.2	44096	4	US-09-949-016-15208	Sequence 15208, A	389	200	22.1	46816	4	US-09-949-016-13493	Sequence 13493, A
C 317	201	22.2	81585	4	US-09-949-016-15427	Sequence 15427, A	390	200	22.1	51273	4	US-09-949-016-13018	Sequence 13018, A
C 318	201	22.2	98828	4	US-09-949-016-16630	Sequence 16630, A	391	200	22.1	52636	4	US-09-949-016-14639	Sequence 14639, A
C 319	201	22.2	108440	4	US-09-949-016-12085	Sequence 12085, A	392	200	22.1	64137	4	US-09-949-016-14631	Sequence 14631, A

C 393	200	22.1	64171	4	US-09-949-016-12502	Sequence 12502, A	C 466	199	21.9	74914	4	US-09-949-016-12286	Sequence 12286, A
C 394	200	22.1	73395	4	US-09-949-016-15151	Sequence 15151, A	C 467	199	21.9	78491	4	US-09-949-016-15132	Sequence 15132, A
C 395	200	22.1	145320	4	US-09-949-016-15858	Sequence 15858, A	C 468	199	21.9	82125	4	US-09-949-016-13517	Sequence 13517, A
C 396	200	22.1	192700	4	US-09-949-016-11820	Sequence 11820, A	C 469	199	21.9	82125	4	US-09-949-016-13518	Sequence 13518, A
C 397	200	22.1	192704	4	US-09-949-016-11820	Sequence 11820, A	C 470	199	21.9	91831	4	US-09-949-016-15095	Sequence 15095, A
C 398	200	22.1	283538	4	US-09-949-016-13506	Sequence 13506, A	C 471	199	21.9	93510	4	US-09-949-016-13694	Sequence 13694, A
C 399	200	22.1	678533	4	US-09-949-016-14577	Sequence 14577, A	C 472	199	21.9	110266	4	US-09-949-016-14913	Sequence 14913, A
C 400	200	22.1	678533	4	US-09-949-016-14577	Sequence 14577, A	C 473	199	21.9	110266	4	US-09-949-016-14914	Sequence 14914, A
C 401	199.8	22.0	601	4	US-09-949-016-39668	Sequence 39668, A	C 474	199	21.9	110266	4	US-09-949-016-14915	Sequence 14915, A
C 402	199.8	22.0	601	4	US-09-949-016-41315	Sequence 41315, A	C 475	199	21.9	110266	4	US-09-949-016-14916	Sequence 14916, A
C 403	199.8	22.0	601	4	US-09-949-016-43318	Sequence 43318, A	C 476	199	21.9	110266	4	US-09-949-016-14917	Sequence 14917, A
C 404	199.8	22.0	601	4	US-09-949-016-43319	Sequence 43319, A	C 477	199	21.9	110266	4	US-09-949-016-14918	Sequence 14918, A
C 405	199.8	22.0	601	4	US-09-949-016-43547	Sequence 43547, A	C 478	199	21.9	110266	4	US-09-949-016-14919	Sequence 14919, A
C 406	199.8	22.0	601	4	US-09-949-016-43548	Sequence 43548, A	C 479	199	21.9	110266	4	US-09-949-016-14920	Sequence 14920, A
C 407	199.8	22.0	601	4	US-09-949-016-43776	Sequence 43776, A	C 480	199	21.9	110266	4	US-09-949-016-14921	Sequence 14921, A
C 408	199.8	22.0	601	4	US-09-949-016-43777	Sequence 43777, A	C 481	199	21.9	110266	4	US-09-949-016-14922	Sequence 14922, A
C 409	199.8	22.0	601	4	US-09-949-016-47534	Sequence 47534, A	C 482	199	21.9	145928	4	US-09-949-016-16476	Sequence 16476, A
C 410	199.8	22.0	601	4	US-09-949-016-82428	Sequence 82428, A	C 483	199	21.9	145928	4	US-09-949-016-15444	Sequence 15444, A
C 411	199.8	22.0	601	4	US-09-949-016-187598	Sequence 187598, A	C 484	199	21.9	145928	4	US-09-801-876B-3	Sequence 3, Appl1
C 412	199.8	22.0	40546	4	US-09-949-016-12847	Sequence 12847, A	C 485	199	21.9	145928	4	US-10-254-869B-3	Sequence 3, Appl1
C 413	199.8	22.0	40546	4	US-09-949-016-12847	Sequence 12847, A	C 486	199	21.9	145928	4	US-10-667-442-3	Sequence 3, Appl1
C 414	199.8	22.0	41578	4	US-09-949-016-12915	Sequence 12915, A	C 487	199	21.9	145928	4	US-09-949-016-15371	Sequence 15371, A
C 415	199.8	22.0	75480	4	US-09-949-016-15090	Sequence 15090, A	C 488	199	21.9	304533	4	US-09-949-016-15372	Sequence 15372, A
C 416	199.8	22.0	78720	4	US-09-949-016-12710	Sequence 12710, A	C 489	199	21.9	304533	4	US-09-949-016-15373	Sequence 15373, A
C 417	199.8	22.0	78720	4	US-09-949-016-12710	Sequence 12710, A	C 490	199	21.9	601	4	US-09-949-016-18742	Sequence 18742, A
C 418	199.8	22.0	106924	4	US-09-949-016-13834	Sequence 13834, A	C 491	199	21.9	601	4	US-09-949-016-17567	Sequence 17567, A
C 419	199.6	22.0	601	4	US-09-949-016-32182	Sequence 32182, A	C 492	199	21.9	7152	3	US-09-167-681-29	Sequence 29, Appl1
C 420	199.6	22.0	601	4	US-09-949-016-60819	Sequence 60819, A	C 493	199	21.9	20182	4	US-09-949-016-13240	Sequence 13240, A
C 421	199.6	22.0	601	4	US-09-949-016-112131	Sequence 112131, A	C 494	199	21.9	33552	4	US-09-949-016-11799	Sequence 11799, A
C 422	199.6	22.0	601	4	US-09-949-016-146504	Sequence 146504, A	C 495	199	21.9	43950	3	US-09-735-934A-3	Sequence 3, Appl1
C 423	199.6	22.0	601	4	US-09-949-016-147535	Sequence 147535, A	C 496	199	21.9	43950	4	US-10-339-657-3	Sequence 3, Appl1
C 424	199.6	22.0	26314	4	US-09-949-016-16389	Sequence 16389, A	C 497	199	21.9	43950	4	US-10-339-657-3	Sequence 14902, A
C 425	199.6	22.0	32278	4	US-09-949-016-14575	Sequence 14575, A	C 498	199	21.9	54779	4	US-09-949-016-14902	Sequence 27, Appl1
C 426	199.6	22.0	36346	4	US-09-949-016-17543	Sequence 17543, A	C 499	199	21.9	54780	4	US-09-949-001-27	Sequence 39, Appl1
C 427	199.6	22.0	51062	4	US-09-949-016-14725	Sequence 14725, A	C 500	199	21.9	54780	4	US-09-949-016-16792	Sequence 16792, A
C 428	199.6	22.0	105189	4	US-09-949-016-13029	Sequence 13029, A	C 501	199	21.9	55114	4	US-09-949-016-15691	Sequence 15691, A
C 429	199.4	22.0	601	4	US-09-949-016-64118	Sequence 64118, A	C 502	199	21.9	87039	4	US-09-949-016-17561	Sequence 17561, A
C 430	199.4	22.0	601	4	US-09-949-016-70685	Sequence 70685, A	C 503	199	21.9	113379	4	US-09-949-016-17562	Sequence 17562, A
C 431	199.4	22.0	601	4	US-09-949-016-70685	Sequence 70685, A	C 504	199	21.9	113379	4	US-09-949-016-17561	Sequence 17561, A
C 432	199.4	22.0	23826	4	US-09-949-016-16712	Sequence 16712, A	C 505	199	21.9	124480	4	US-09-949-016-15921	Sequence 15921, A
C 433	199.4	22.0	23826	4	US-09-949-016-16713	Sequence 16713, A	C 506	199	21.9	223471	4	US-09-949-016-12387	Sequence 12387, A
C 434	199.4	22.0	23826	4	US-09-949-016-16714	Sequence 16714, A	C 507	199	21.9	223471	4	US-09-949-016-12784	Sequence 12784, A
C 435	199.4	22.0	23826	4	US-09-949-016-16715	Sequence 16715, A	C 508	199	21.9	223471	4	US-09-949-016-12725	Sequence 12725, A
C 436	199.4	22.0	43192	4	US-09-949-016-15665	Sequence 15665, A	C 509	199	21.9	276687	4	US-09-949-016-13840	Sequence 13840, A
C 437	199.4	22.0	93971	4	US-09-949-016-16097	Sequence 16097, A	C 510	199	21.9	601	4	US-09-949-016-76001	Sequence 76001, A
C 438	199.4	22.0	93971	4	US-09-949-016-16098	Sequence 16098, A	C 511	199	21.9	601	4	US-09-949-016-127637	Sequence 127637, A
C 439	199.4	22.0	145928	4	US-09-949-016-15444	Sequence 15444, A	C 512	199	21.9	601	4	US-09-949-016-127974	Sequence 127974, A
C 440	199.4	22.0	176006	4	US-09-949-016-16804	Sequence 16804, A	C 513	199	21.9	601	4	US-09-949-016-131654	Sequence 131654, A
C 441	199.4	22.0	253375	4	US-09-949-016-12849	Sequence 12849, A	C 514	199	21.9	1946	4	US-09-620-312D-462	Sequence 462, App
C 442	199.2	22.0	601	4	US-09-949-016-69950	Sequence 69950, A	C 515	199	21.9	15297	3	US-09-817-180-3	Sequence 3, Appl1
C 443	199.2	22.0	29907	4	US-09-949-016-13395	Sequence 13395, A	C 516	199	21.9	15297	4	US-10-003-295-3	Sequence 3, Appl1
C 444	199.2	22.0	29913	4	US-09-949-016-12481	Sequence 12481, A	C 517	199	21.9	45183	4	US-09-949-016-12798	Sequence 12798, A
C 445	199.2	22.0	31820	4	US-09-949-016-13356	Sequence 13356, A	C 518	199	21.9	52789	4	US-09-949-016-12130	Sequence 12130, A
C 446	199.2	22.0	37215	4	US-09-949-016-15526	Sequence 15526, A	C 519	199	21.9	52790	4	US-09-949-016-16641	Sequence 16641, A
C 447	199.2	22.0	91279	4	US-09-949-016-15146	Sequence 15146, A	C 520	199	21.9	52790	4	US-09-949-016-11933	Sequence 11933, A
C 448	199.2	22.0	100463	4	US-09-949-016-12511	Sequence 12511, A	C 521	199	21.9	52790	4	US-09-949-016-14735	Sequence 14735, A
C 449	199.2	22.0	100468	4	US-09-949-016-13725	Sequence 13725, A	C 522	199	21.9	60137	4	US-09-949-016-14912	Sequence 14912, A
C 450	199.2	22.0	194537	4	US-09-949-016-13928	Sequence 13928, A	C 523	199	21.9	67581	4	US-09-949-016-14768	Sequence 14768, A
C 451	199.2	22.0	201529	4	US-09-949-016-12740	Sequence 12740, A	C 524	199	21.9	67643	4	US-09-949-016-14760	Sequence 14760, A
C 452	199.2	22.0	304533	4	US-09-949-016-15371	Sequence 15371, A	C 525	199	21.9	82612	4	US-09-949-016-16803	Sequence 16803, A
C 453	199.2	22.0	304533	4	US-09-949-016-15372	Sequence 15372, A	C 526	199	21.9	90724	4	US-09-949-016-16601	Sequence 16601, A
C 454	199	21.9	601	4	US-09-949-016-61837	Sequence 61837, A	C 527	199	21.9	96922	4	US-09-949-016-17061	Sequence 17061, A
C 455	199	21.9	8374	4	US-09-949-016-15257	Sequence 15257, A	C 528	199	21.9	97195	4	US-09-949-016-12212	Sequence 12212, A
C 456	199	21.9	10546	4	US-09-949-016-15624	Sequence 15624, A	C 529	199	21.9	97196	4	US-09-949-016-16971	Sequence 16971, A
C 457	199	21.9	17154	4	US-09-949-016-16889	Sequence 16889, A	C 530	199	21.9	96962	4	US-09-949-016-14325	Sequence 14325, A
C 458	199	21.9	19503	4	US-09-949-016-16528	Sequence 16528, A	C 531	199	21.9	102053	4	US-09-949-016-13013	Sequence 13013, A
C 459	199	21.9	24205	4	US-09-949-016-15385	Sequence 15385, A	C 532	199	21.9	102084	4	US-09-949-016-17100	Sequence 17100, A
C 460	199	21.9	39982	4	US-09-820-924-3	Sequence 3, Appl1	C 533	199	21.9	112283	4	US-09-949-016-16976	Sequence 16976, A
C 461	199	21.9	39982	4	US-10-369-626-3	Sequence 3, Appl1	C 534	199	21.9	112283	4	US-09-949-016-16977	Sequence 16977, A
C 462	199	21.9	40493	4	US-09-949-016-15453	Sequence 15453, A	C 535	199	21.9	11649	4	US-09-949-016-12537	Sequence 12537, A
C 463	199	21.9	51046	4	US-09-949-016-12739	Sequence 12739, A	C 536	199	21.9	11649	4	US-09-949-016-12982	Sequence 12982, A
C 464	199	21.9	51046	4	US-09-949-016-13946	Sequence 13946, A	C 537	199	21.9	157866	4	US-09-949-016-12983	Sequence 12983, A
C 465	199	21.9	74881	4	US-09-949-016-15545	Sequence 15545, A	C 538	199	21.9	157866	4	US-09-949-016-12984	Sequence 12984, A

C 539	198.4	21.9	601	4	US-09-949-016-150106	Sequence 150106,	C 612	198	21.8	601	4	US-09-949-016-44634	Sequence 44634, A
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542	198.4	21.9	601	4	US-09-949-016-171235	Sequence 171235,	615	198	21.8	601	4	US-09-949-016-140034	Sequence 140034,
543	198.4	21.9	7705	2	US-08-687-080-115	Sequence 115, App	616	198	21.8	601	4	US-09-949-016-150107	Sequence 150107,
544	198.4	21.9	15586	4	US-09-949-016-13899	Sequence 13899, A	617	198	21.8	601	4	US-09-949-016-160816	Sequence 160816,
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550	198.4	21.9	50797	4	US-09-949-016-16346	Sequence 16346, A	623	198	21.8	33731	4	US-09-949-016-13473	Sequence 13473, A
551	198.4	21.9	50797	4	US-09-949-016-16347	Sequence 16347, A	624	198	21.8	33731	4	US-09-949-016-13474	Sequence 13474, A
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553	198.4	21.9	72278	4	US-09-949-016-16113	Sequence 16113, A	626	198	21.8	38814	4	US-09-949-016-13471	Sequence 13471, A
554	198.4	21.9	85854	4	US-09-949-016-12908	Sequence 12908, A	627	198	21.8	38814	4	US-09-949-016-13471	Sequence 13471, A
555	198.4	21.9	107239	4	US-09-949-016-12663	Sequence 12663, A	628	198	21.8	39528	4	US-09-949-016-15475	Sequence 15475, A
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558	198.4	21.9	107330	4	US-09-949-016-15409	Sequence 15409, A	631	198	21.8	44019	4	US-09-949-016-14902	Sequence 14902, A
559	198.4	21.9	107330	4	US-09-949-016-15410	Sequence 15410, A	632	198	21.8	51336	4	US-09-949-016-16054	Sequence 16054, A
560	198.4	21.9	107330	4	US-09-949-016-15411	Sequence 15411, A	633	198	21.8	51336	4	US-09-949-016-16054	Sequence 16054, A
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562	198.4	21.9	107750	4	US-09-949-016-13412	Sequence 13412, A	635	198	21.8	76399	4	US-09-949-016-16819	Sequence 16819, A
563	198.4	21.9	107751	4	US-09-949-016-15413	Sequence 15413, A	636	198	21.8	85963	4	US-09-949-016-11804	Sequence 11804, A
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569	198.4	21.9	107926	4	US-09-949-016-15406	Sequence 15406, A	642	197.8	21.8	601	4	US-09-949-016-131748	Sequence 131748, A
570	198.4	21.9	107926	4	US-09-949-016-15407	Sequence 15407, A	643	197.8	21.8	601	4	US-09-949-016-148576	Sequence 148576, A
571	198.4	21.9	133358	4	US-09-949-016-16964	Sequence 16964, A	644	197.8	21.8	601	4	US-09-949-016-148576	Sequence 148576, A
572	198.4	21.9	133360	4	US-09-949-016-12651	Sequence 12651, A	645	197.8	21.8	6129	4	US-09-949-016-176106	Sequence 176106, A
573	198.4	21.9	143971	4	US-09-949-016-13590	Sequence 13590, A	646	197.8	21.8	8412	4	US-09-949-016-15708	Sequence 15708, A
574	198.4	21.9	149143	4	US-09-949-016-16144	Sequence 16144, A	647	197.8	21.8	12797	4	US-09-949-016-16798	Sequence 16798, A
575	198.4	21.9	268449	4	US-09-949-016-17244	Sequence 17244, A	648	197.8	21.8	15778	4	US-09-949-016-13538	Sequence 13538, A
576	198.4	21.9	601	4	US-09-949-016-33302	Sequence 33302, A	649	197.8	21.8	18620	4	US-09-949-016-13010	Sequence 13010, A
577	198.2	21.9	601	4	US-09-949-016-33303	Sequence 33303, A	650	197.8	21.8	18620	4	US-09-949-016-11853	Sequence 11853, A
578	198.2	21.9	601	4	US-09-949-016-33304	Sequence 33304, A	651	197.8	21.8	24523	4	US-09-949-016-15707	Sequence 15707, A
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580	198.2	21.9	601	4	US-09-949-016-82427	Sequence 82427, A	653	197.8	21.8	53526	3	US-08-658-136-2	Sequence 2, App1
581	198.2	21.9	601	4	US-09-949-016-137405	Sequence 137405, A	654	197.8	21.8	53577	3	US-08-658-136-1	Sequence 1, App1
582	198.2	21.9	601	4	US-09-949-016-167373	Sequence 167373, A	655	197.8	21.8	56904	4	US-09-949-016-15501	Sequence 15501, A
583	198.2	21.9	601	4	US-09-949-016-176953	Sequence 176953, A	656	197.8	21.8	80411	4	US-09-949-016-15777	Sequence 15777, A
584	198.2	21.9	601	4	US-09-949-016-186050	Sequence 186050, A	657	197.8	21.8	92304	4	US-09-949-016-15943	Sequence 15943, A
585	198.2	21.9	601	4	US-09-949-016-187597	Sequence 187597, A	658	197.8	21.8	98302	4	US-09-949-016-16847	Sequence 16847, A
586	198.2	21.9	14345	4	US-09-949-016-15449	Sequence 15449, A	659	197.8	21.8	112507	4	US-09-949-016-16240	Sequence 16240, A
587	198.2	21.9	21535	4	US-09-949-016-12826	Sequence 12826, A	660	197.8	21.8	112507	4	US-09-949-016-12794	Sequence 12794, A
588	198.2	21.9	21535	4	US-09-949-016-12827	Sequence 12827, A	661	197.8	21.8	112507	4	US-09-949-016-12794	Sequence 12794, A
589	198.2	21.9	21535	4	US-09-949-016-12828	Sequence 12828, A	662	197.8	21.8	112508	4	US-09-949-016-16589	Sequence 16589, A
590	198.2	21.9	21535	4	US-09-949-016-12829	Sequence 12829, A	663	197.8	21.8	112508	4	US-09-949-016-16590	Sequence 16590, A
591	198.2	21.9	21536	4	US-09-949-016-13366	Sequence 13366, A	664	197.8	21.8	137949	4	US-09-949-016-12196	Sequence 12196, A
592	198.2	21.9	21536	4	US-09-949-016-13367	Sequence 13367, A	665	197.8	21.8	137956	4	US-09-949-016-12196	Sequence 12196, A
593	198.2	21.9	21536	4	US-09-949-016-13368	Sequence 13368, A	666	197.8	21.8	143155	4	US-09-949-016-11925	Sequence 11925, A
594	198.2	21.9	21536	4	US-09-949-016-13369	Sequence 13369, A	667	197.8	21.8	143156	4	US-09-949-016-14368	Sequence 14368, A
595	198.2	21.9	22634	4	US-09-949-016-16666	Sequence 16666, A	668	197.8	21.8	143156	4	US-09-949-016-14368	Sequence 14368, A
596	198.2	21.9	36180	4	US-09-949-016-11745	Sequence 11745, A	669	197.8	21.8	157832	4	US-09-949-016-16723	Sequence 16723, A
597	198.2	21.9	36181	4	US-09-949-016-16163	Sequence 16163, A	670	197.8	21.8	162480	3	US-09-345-882-1	Sequence 1, App1
598	198.2	21.9	36228	4	US-09-949-016-12256	Sequence 12256, A	671	197.8	21.8	189560	4	US-09-949-016-11702	Sequence 11702, A
599	198.2	21.9	36228	4	US-09-949-016-15468	Sequence 15468, A	672	197.8	21.8	198942	4	US-09-949-016-13709	Sequence 13709, A
600	198.2	21.9	39243	4	US-09-949-016-12316	Sequence 12316, A	673	197.8	21.8	246444	4	US-09-949-016-13113	Sequence 13113, A
601	198.2	21.9	39243	4	US-09-949-016-15443	Sequence 15443, A	674	197.8	21.8	325791	4	US-09-949-016-13113	Sequence 13113, A
602	198.2	21.9	44988	4	US-09-949-016-16344	Sequence 16344, A	675	197.6	21.8	601	4	US-09-949-016-69951	Sequence 69951, A
603	198.2	21.9	47787	4	US-09-949-016-11999	Sequence 11999, A	676	197.6	21.8	601	4	US-09-949-016-115572	Sequence 115572, A
604	198.2	21.9	84870	4	US-09-949-016-17347	Sequence 17347, A	677	197.6	21.8	601	4	US-09-949-016-115665	Sequence 115665, A
605	198.2	21.9	96074	4	US-09-949-016-12760	Sequence 12760, A	678	197.6	21.8	601	4	US-09-949-016-115758	Sequence 115758, A
606	198.2	21.9	96074	4	US-09-949-016-12760	Sequence 12760, A	679	197.6	21.8	601	4	US-09-949-016-11851	Sequence 11851, A
607	198.2	21.9	96074	4	US-09-949-016-13611	Sequence 13611, A	680	197.6	21.8	601	4	US-09-949-016-11851	Sequence 11851, A
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610	198	21.8	601	4	US-09-949-016-33412	Sequence 33412, A	683	197.6	21.8	601	4	US-09-949-016-116223	Sequence 116223, A
611	198	21.8	601	4	US-09-949-016-41047	Sequence 41047, A	684	197.6	21.8	601	4	US-09-949-016-116316	Sequence 116316, A

C 685	197.6	21.8	601	4	US-09-949-016-116409	Sequence 116409,	758	197.2	21.7	41125	4	US-09-949-016-12413	Sequence 12413, A
C 686	197.6	21.8	601	4	US-09-949-016-1176518	Sequence 1176518,	759	197.2	21.7	41126	4	US-09-949-016-117273	Sequence 117273, A
C 687	197.6	21.8	26611	4	US-09-949-016-164884	Sequence 164884, A	760	197.2	21.7	61461	4	US-09-949-016-15419	Sequence 15419, A
C 688	197.6	21.8	38808	4	US-09-949-016-11802	Sequence 11802, A	761	197.2	21.7	62908	4	US-09-949-016-17554	Sequence 17554, A
C 689	197.6	21.8	38808	4	US-09-949-016-16735	Sequence 16735, A	762	197.2	21.7	76610	4	US-09-949-016-15521	Sequence 15521, A
C 690	197.6	21.8	46433	4	US-09-949-016-16824	Sequence 16824, A	763	197.2	21.7	83697	4	US-09-949-016-16040	Sequence 16040, A
C 691	197.6	21.8	53108	4	US-09-949-016-16681	Sequence 16681, A	764	197.2	21.7	85854	4	US-09-949-016-12908	Sequence 12908, A
C 692	197.6	21.8	59139	4	US-09-949-016-16115	Sequence 16115, A	765	197.2	21.7	92139	4	US-09-918-686-1	Sequence 1, Appl1
C 693	197.6	21.8	66164	4	US-09-949-016-13574	Sequence 13574, A	766	197.2	21.7	197875	4	US-09-949-016-15425	Sequence 15425, A
C 694	197.6	21.8	119762	4	US-09-949-016-17313	Sequence 17313, A	767	197.2	21.7	248688	4	US-09-949-016-12614	Sequence 12614, A
C 695	197.6	21.8	119981	4	US-09-949-016-11844	Sequence 11844, A	768	197	21.7	601	4	US-09-949-016-78179	Sequence 78179, A
C 696	197.6	21.8	119982	4	US-09-949-016-13606	Sequence 13606, A	769	197	21.7	601	4	US-09-949-016-113846	Sequence 113846, A
C 697	197.6	21.8	139150	4	US-09-949-016-17398	Sequence 17398, A	770	197	21.7	601	4	US-09-949-016-114014	Sequence 114014, A
C 698	197.6	21.8	139577	4	US-09-949-016-12879	Sequence 12879, A	771	197	21.7	601	4	US-09-949-016-114182	Sequence 114182, A
C 699	197.6	21.8	194915	4	US-09-949-016-15584	Sequence 15584, A	772	197	21.7	601	4	US-09-949-016-114350	Sequence 114350, A
C 700	197.6	21.8	300402	4	US-09-949-016-13432	Sequence 13432, A	773	197	21.7	601	4	US-09-949-016-114518	Sequence 114518, A
C 701	197.4	21.8	601	4	US-09-949-016-21510	Sequence 21510, A	774	197	21.7	601	4	US-09-949-016-114686	Sequence 114686, A
C 702	197.4	21.8	601	4	US-09-949-016-36770	Sequence 36770, A	775	197	21.7	601	4	US-09-949-016-114854	Sequence 114854, A
C 703	197.4	21.8	601	4	US-09-949-016-91427	Sequence 91427, A	776	197	21.7	601	4	US-09-949-016-114854	Sequence 114854, A
C 704	197.4	21.8	601	4	US-09-949-016-91499	Sequence 91499, A	777	197	21.7	8396	3	US-09-328-174A-1	Sequence 1, Appl1
C 705	197.4	21.8	601	4	US-09-949-016-122955	Sequence 122955, A	778	197	21.7	8409	3	US-09-167-681-37	Sequence 37, Appl1
C 706	197.4	21.8	601	4	US-09-949-016-123049	Sequence 123049, A	779	197	21.7	15615	4	US-09-949-016-17221	Sequence 17221, A
C 707	197.4	21.8	601	4	US-09-949-016-123143	Sequence 123143, A	780	197	21.7	18819	4	US-09-949-016-17446	Sequence 17446, A
C 708	197.4	21.8	601	4	US-09-949-016-123237	Sequence 123237, A	781	197	21.7	20610	4	US-09-949-016-14610	Sequence 14610, A
C 709	197.4	21.8	601	4	US-09-949-016-123331	Sequence 123331, A	782	197	21.7	33227	4	US-09-949-016-14108	Sequence 14108, A
C 710	197.4	21.8	601	4	US-09-949-016-123373	Sequence 123373, A	783	197	21.7	34548	4	US-09-949-016-12681	Sequence 12681, A
C 711	197.4	21.8	601	4	US-09-949-016-123415	Sequence 123415, A	784	197	21.7	34548	4	US-09-949-016-16124	Sequence 16124, A
C 712	197.4	21.8	601	4	US-09-949-016-123459	Sequence 123459, A	785	197	21.7	39032	4	US-09-949-016-12874	Sequence 12874, A
C 713	197.4	21.8	601	4	US-09-949-016-123499	Sequence 123499, A	786	197	21.7	39039	4	US-09-949-016-15462	Sequence 15462, A
C 714	197.4	21.8	601	4	US-09-949-016-123541	Sequence 123541, A	787	197	21.7	41639	4	US-09-949-016-15471	Sequence 15471, A
C 715	197.4	21.8	601	4	US-09-949-016-123583	Sequence 123583, A	788	197	21.7	44608	4	US-09-949-016-15604	Sequence 15604, A
C 716	197.4	21.8	601	4	US-09-949-016-123625	Sequence 123625, A	789	197	21.7	44971	4	US-09-949-016-17049	Sequence 17049, A
C 717	197.4	21.8	601	4	US-09-949-016-123667	Sequence 123667, A	790	197	21.7	56665	4	US-09-949-016-14026	Sequence 14026, A
C 718	197.4	21.8	601	4	US-09-949-016-123709	Sequence 123709, A	791	197	21.7	60424	4	US-09-949-016-12175	Sequence 12175, A
C 719	197.4	21.8	601	4	US-09-949-016-123751	Sequence 123751, A	792	197	21.7	65300	4	US-09-949-016-16813	Sequence 16813, A
C 720	197.4	21.8	601	4	US-09-949-016-138053	Sequence 138053, A	793	197	21.7	66328	4	US-09-949-016-12917	Sequence 12917, A
C 721	197.4	21.8	601	4	US-09-949-016-154829	Sequence 154829, A	794	197	21.7	77535	4	US-09-949-016-14280	Sequence 14280, A
C 722	197.4	21.8	601	4	US-09-949-016-171104	Sequence 171104, A	795	197	21.7	77535	4	US-09-949-016-14281	Sequence 14281, A
C 723	197.4	21.8	601	4	US-09-949-016-171234	Sequence 171234, A	796	197	21.7	107421	4	US-09-949-016-15532	Sequence 15532, A
C 724	197.4	21.8	601	4	US-09-949-016-178113	Sequence 178113, A	797	197	21.7	121982	4	US-09-949-016-12085	Sequence 12085, A
C 725	197.4	21.8	15148	4	US-09-949-016-15858	Sequence 15858, A	798	197	21.7	121982	4	US-09-949-016-14105	Sequence 14105, A
C 726	197.4	21.8	27555	4	US-09-949-016-17466	Sequence 17466, A	799	197	21.7	121982	4	US-09-949-016-14105	Sequence 14105, A
C 727	197.4	21.8	31469	4	US-09-949-016-13722	Sequence 13722, A	800	197	21.7	13791	4	US-09-949-016-15092	Sequence 15092, A
C 728	197.4	21.8	34330	4	US-09-949-016-12052	Sequence 12052, A	801	196.8	21.7	601	4	US-09-949-016-13023	Sequence 13023, A
C 729	197.4	21.8	38954	4	US-09-949-016-12292	Sequence 12292, A	802	196.8	21.7	601	4	US-09-949-016-18079	Sequence 18079, A
C 730	197.4	21.8	79350	4	US-09-949-016-12467	Sequence 12467, A	803	196.8	21.7	601	4	US-09-949-016-190491	Sequence 190491, A
C 731	197.4	21.8	79351	4	US-09-949-016-16275	Sequence 16275, A	804	196.8	21.7	601	4	US-09-949-016-162049	Sequence 162049, A
C 732	197.4	21.8	84875	4	US-09-949-016-17334	Sequence 17334, A	805	196.8	21.7	13948	4	US-09-949-016-165965	Sequence 165965, A
C 733	197.4	21.8	84875	4	US-09-949-016-17335	Sequence 17335, A	806	196.8	21.7	13948	4	US-09-949-016-13061	Sequence 13061, A
C 734	197.4	21.8	84875	4	US-09-949-016-17336	Sequence 17336, A	807	196.8	21.7	13948	4	US-09-949-016-17612	Sequence 17612, A
C 735	197.4	21.8	84875	4	US-09-949-016-17337	Sequence 17337, A	808	196.8	21.7	27659	4	US-09-949-016-17612	Sequence 17612, A
C 736	197.4	21.8	85152	4	US-09-949-016-12665	Sequence 12665, A	809	196.8	21.7	28321	4	US-09-949-016-11936	Sequence 11936, A
C 737	197.4	21.8	85152	4	US-09-949-016-12667	Sequence 12667, A	810	196.8	21.7	28325	4	US-09-949-016-16622	Sequence 16622, A
C 738	197.4	21.8	85152	4	US-09-949-016-12667	Sequence 12667, A	811	196.8	21.7	35417	4	US-09-949-016-16129	Sequence 16129, A
C 739	197.4	21.8	85152	4	US-09-949-016-12668	Sequence 12668, A	812	196.8	21.7	41617	4	US-09-949-016-14356	Sequence 14356, A
C 740	197.4	21.8	96645	4	US-09-949-016-13658	Sequence 13658, A	813	196.8	21.7	41618	4	US-09-949-016-14356	Sequence 14356, A
C 741	197.4	21.8	1284780	4	US-09-949-016-13765	Sequence 13765, A	814	196.8	21.7	43463	4	US-09-949-016-16341	Sequence 16341, A
C 742	197.4	21.8	192506	4	US-09-949-016-15127	Sequence 15127, A	815	196.8	21.7	44052	4	US-09-949-016-12203	Sequence 12203, A
C 743	197.4	21.8	192506	4	US-09-949-016-15830	Sequence 15830, A	816	196.8	21.7	54878	4	US-09-949-016-12255	Sequence 12255, A
C 744	197.4	21.8	300402	4	US-09-949-016-13632	Sequence 13632, A	817	196.8	21.7	70000	3	US-09-851-896-3	Sequence 3, Appl1
C 745	197.4	21.8	300598	4	US-09-949-016-11868	Sequence 11868, A	818	196.8	21.7	75704	4	US-09-949-016-15580	Sequence 15580, A
C 746	197.4	21.8	302604	4	US-09-949-016-14589	Sequence 14589, A	819	196.8	21.7	72992	4	US-09-949-016-17592	Sequence 17592, A
C 747	197.4	21.8	302604	4	US-09-949-016-14589	Sequence 14589, A	820	196.8	21.7	76399	4	US-09-949-016-16819	Sequence 16819, A
C 748	197.4	21.8	308962	4	US-09-949-016-17119	Sequence 17119, A	821	196.8	21.7	78846	4	US-09-949-016-12396	Sequence 12396, A
C 749	197.2	21.7	282	1	US-08-133-629-8	Sequence 8, Appl1	822	196.8	21.7	78846	4	US-09-949-016-12791	Sequence 12791, A
C 750	197.2	21.7	449	1	US-09-621-976-16908	Sequence 16908, A	823	196.8	21.7	78846	4	US-09-949-016-12792	Sequence 12792, A
C 751	197.2	21.7	601	4	US-09-949-016-184729	Sequence 184729, A	824	196.8	21.7	78846	4	US-09-949-016-12793	Sequence 12793, A
C 752	197.2	21.7	7654	4	US-09-953-318-20	Sequence 20, Appl1	825	196.8	21.7	78850	4	US-09-949-016-16013	Sequence 16013, A
C 753	197.2	21.7	31229	4	US-09-949-016-17610	Sequence 17610, A	826	196.8	21.7	78850	4	US-09-949-016-16014	Sequence 16014, A
C 754	197.2	21.7	31231	4	US-09-949-016-12619	Sequence 12619, A	827	196.8	21.7	78850	4	US-09-949-016-16015	Sequence 16015, A
C 755	197.2	21.7	40936	4	US-09-949-016-15766	Sequence 15766, A	828	196.8	21.7	78850	4	US-09-949-016-16016	Sequence 16016, A
C 756	197.2	21.7	40936	4	US-09-949-016-16607	Sequence 16607, A	829	196.8	21.7	78850	4	US-09-949-016-16201	Sequence 16201, A
C 757	197.2	21.7	40936	4	US-09-949-016-16608	Sequence 16608, A	830	196.8	21.7	78850	4	US-09-949-016-16202	Sequence 16202, A

831	196.8	21.7	78850	4	US-09-949-016-16203	Sequence 16203, A	904	196.4	21.7	601	4	US-09-949-016-171106	Sequence 171106,
832	196.8	21.7	78850	4	US-09-949-016-16204	Sequence 16204, A	905	196.4	21.7	601	4	US-09-949-016-171236	Sequence 171236,
833	196.8	21.7	79350	4	US-09-949-016-16267	Sequence 12467, A	906	196.4	21.7	601	4	US-09-949-016-175176	Sequence 175176,
834	196.8	21.7	79351	4	US-09-949-016-16275	Sequence 16275, A	907	196.4	21.7	601	4	US-09-949-016-175187	Sequence 175187,
835	196.8	21.7	80858	4	US-09-949-016-16259	Sequence 12659, A	908	196.4	21.7	601	4	US-09-949-016-175188	Sequence 175188,
836	196.8	21.7	80859	4	US-09-949-016-16259	Sequence 12659, A	909	196.4	21.7	601	4	US-09-949-016-175209	Sequence 175209,
837	196.8	21.7	90472	4	US-09-949-016-14038	Sequence 14038, A	910	196.4	21.7	14185	4	US-09-949-016-14809	Sequence 14809, A
838	196.8	21.7	93493	4	US-09-949-016-12063	Sequence 12063, A	911	196.4	21.7	14754	4	US-09-949-016-13636	Sequence 13636, A
839	196.8	21.7	95020	4	US-09-949-016-13272	Sequence 13272, A	912	196.4	21.7	17085	4	US-09-949-016-15507	Sequence 15507, A
840	196.8	21.7	104077	4	US-09-949-016-15393	Sequence 15393, A	913	196.4	21.7	20562	4	US-09-949-016-16074	Sequence 16072, A
841	196.8	21.7	149543	4	US-09-949-016-15347	Sequence 15347, A	914	196.4	21.7	25166	4	US-09-949-016-15792	Sequence 15792, A
842	196.8	21.7	260286	4	US-09-949-016-17037	Sequence 12106, A	915	196.4	21.7	29686	4	US-09-949-016-13729	Sequence 13724, A
843	196.8	21.7	260293	4	US-09-949-016-12106	Sequence 12505, A	916	196.4	21.7	30782	4	US-09-949-016-13724	Sequence 13724, A
844	196.8	21.7	670689	4	US-09-949-016-12505	Sequence 14207, A	917	196.4	21.7	31668	4	US-09-949-016-11314	Sequence 13114, A
845	196.8	21.7	670690	4	US-09-949-016-14207	Sequence 14207, A	918	196.4	21.7	31668	4	US-09-949-016-11307	Sequence 11907, A
846	196.6	21.7	461	3	US-09-404-879A-1	Sequence 1, Appl1	919	196.4	21.7	40897	4	US-09-949-016-13910	Sequence 13910, A
847	196.6	21.7	461	3	US-09-404-879A-3	Sequence 3, Appl1	920	196.4	21.7	40897	4	US-09-949-016-13911	Sequence 13911, A
848	196.6	21.7	461	4	US-09-338-933-1	Sequence 3, Appl1	921	196.4	21.7	40897	4	US-09-949-016-13912	Sequence 13912, A
849	196.6	21.7	461	4	US-09-338-933-3	Sequence 3, Appl1	922	196.4	21.7	40897	4	US-09-949-016-13913	Sequence 13913, A
850	196.6	21.7	461	4	US-09-215-681-1	Sequence 1, Appl1	923	196.4	21.7	40897	4	US-09-949-016-14410	Sequence 14410, A
851	196.6	21.7	461	4	US-09-215-681-3	Sequence 3, Appl1	924	196.4	21.7	40897	4	US-09-949-016-14411	Sequence 14411, A
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853	196.6	21.7	461	4	US-09-216-003A-1	Sequence 1, Appl1	926	196.4	21.7	40897	4	US-09-949-016-14413	Sequence 14413, A
854	196.6	21.7	461	4	US-09-667-857-1	Sequence 3, Appl1	927	196.4	21.7	40897	4	US-09-949-016-14409	Sequence 14409, A
855	196.6	21.7	461	4	US-09-667-857-3	Sequence 3, Appl1	928	196.4	21.7	40897	4	US-09-949-016-14410	Sequence 14410, A
856	196.6	21.7	601	4	US-09-949-016-163002	Sequence 163002, A	929	196.4	21.7	65990	4	US-09-949-016-12630	Sequence 12630, A
857	196.6	21.7	601	4	US-09-949-016-167371	Sequence 167371, A	930	196.4	21.7	66627	4	US-09-949-016-16112	Sequence 16112, A
858	196.6	21.7	601	4	US-09-949-016-167372	Sequence 167372, A	931	196.4	21.7	82494	4	US-09-949-016-16137	Sequence 16937, A
859	196.6	21.7	601	4	US-09-949-016-191418	Sequence 191418, A	932	196.4	21.7	82494	4	US-09-949-016-15096	Sequence 15096, A
860	196.6	21.7	4014	4	US-09-949-016-4648	Sequence 4648, Ap	933	196.4	21.7	93778	4	US-09-949-016-14913	Sequence 14913, A
861	196.6	21.7	4014	4	US-09-949-016-4649	Sequence 4649, Ap	934	196.4	21.7	110266	4	US-09-949-016-14914	Sequence 14914, A
862	196.6	21.7	12394	3	US-09-488-856A-10	Sequence 10, Appl1	935	196.4	21.7	110266	4	US-09-949-016-14915	Sequence 14915, A
863	196.6	21.7	14781	4	US-09-949-016-15917	Sequence 15917, A	936	196.4	21.7	110266	4	US-09-949-016-14916	Sequence 14916, A
864	196.6	21.7	15108	4	US-09-949-016-15918	Sequence 15918, A	937	196.4	21.7	110266	4	US-09-949-016-14917	Sequence 14917, A
865	196.6	21.7	15108	4	US-09-949-016-17205	Sequence 17205, A	938	196.4	21.7	110266	4	US-09-949-016-14918	Sequence 14918, A
866	196.6	21.7	15108	4	US-09-949-016-16380	Sequence 16380, A	939	196.4	21.7	110266	4	US-09-949-016-14919	Sequence 14919, A
867	196.6	21.7	16346	4	US-09-949-016-15574	Sequence 15574, A	940	196.4	21.7	110266	4	US-09-949-016-14920	Sequence 14920, A
868	196.6	21.7	17488	4	US-09-949-016-13163	Sequence 13163, A	941	196.4	21.7	110266	4	US-09-949-016-14921	Sequence 14921, A
869	196.6	21.7	18302	4	US-09-949-016-16752	Sequence 16752, A	942	196.4	21.7	110266	4	US-09-949-016-14922	Sequence 14922, A
870	196.6	21.7	20347	4	US-09-949-016-15149	Sequence 15149, A	943	196.4	21.7	110266	4	US-09-949-016-14923	Sequence 14923, A
871	196.6	21.7	20942	4	US-09-949-016-15149	Sequence 15149, A	944	196.4	21.7	110266	4	US-09-949-016-14924	Sequence 14924, A
872	196.6	21.7	29165	4	US-09-949-016-12303	Sequence 12303, A	945	196.4	21.7	113042	4	US-09-949-016-15246	Sequence 15246, A
873	196.6	21.7	32393	4	US-09-949-016-14203	Sequence 14203, A	946	196.4	21.7	113042	4	US-09-949-016-15247	Sequence 15247, A
874	196.6	21.7	33155	4	US-09-949-016-16421	Sequence 16421, A	947	196.4	21.7	121982	4	US-09-949-016-14105	Sequence 14105, A
875	196.6	21.7	33519	4	US-09-949-016-17165	Sequence 17165, A	948	196.4	21.7	121982	4	US-09-949-016-14106	Sequence 14106, A
876	196.6	21.7	35337	4	US-09-949-016-17249	Sequence 17249, A	949	196.4	21.7	121982	4	US-09-949-016-14107	Sequence 14107, A
877	196.6	21.7	36791	4	US-09-949-016-16380	Sequence 16380, A	950	196.4	21.7	181251	4	US-09-949-016-15970	Sequence 15970, A
878	196.6	21.7	36791	4	US-09-949-016-16381	Sequence 16381, A	951	196.4	21.7	181251	4	US-09-949-016-15971	Sequence 15971, A
879	196.6	21.7	38954	4	US-09-949-016-12282	Sequence 12282, A	952	196.4	21.7	26465	4	US-09-949-016-25029	Sequence 25029, A
880	196.6	21.7	42479	4	US-09-949-016-16631	Sequence 16631, A	953	196.4	21.7	26465	4	US-09-949-016-25030	Sequence 25030, A
881	196.6	21.7	42479	4	US-09-949-016-16632	Sequence 16632, A	954	196.4	21.7	26465	4	US-09-949-016-25031	Sequence 25031, A
882	196.6	21.7	42479	4	US-09-949-016-17555	Sequence 17555, A	955	196.4	21.7	26465	4	US-09-949-016-25032	Sequence 25032, A
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884	196.6	21.7	46841	4	US-09-949-016-13466	Sequence 13466, A	957	196.4	21.7	26465	4	US-09-949-016-25034	Sequence 25034, A
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886	196.6	21.7	53769	4	US-09-949-016-17527	Sequence 17527, A	959	196.4	21.7	26465	4	US-09-949-016-25036	Sequence 25036, A
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888	196.6	21.7	62804	4	US-10-096-960-3	Sequence 3, Appl1	961	196.4	21.7	601	4	US-09-949-016-148594	Sequence 148594, A
889	196.6	21.7	88557	4	US-09-949-016-17028	Sequence 17028, A	962	196.4	21.7	6299	4	US-09-949-016-166297	Sequence 166297, A
890	196.6	21.7	93398	4	US-09-949-016-14167	Sequence 14167, A	963	196.4	21.7	17633	4	US-09-949-016-13137	Sequence 13137, A
891	196.6	21.7	99500	3	US-09-798-096-10	Sequence 10, Appl1	964	196.4	21.7	19567	4	US-09-949-016-12096	Sequence 12096, A
892	196.6	21.7	118143	4	US-09-949-016-17196	Sequence 17196, A	965	196.4	21.7	22311	4	US-09-949-016-14114	Sequence 14114, A
893	196.6	21.7	129658	4	US-09-949-016-17195	Sequence 17195, A	966	196.4	21.7	22311	4	US-09-949-016-12244	Sequence 12244, A
894	196.6	21.7	152481	4	US-09-949-016-12521	Sequence 12521, A	967	196.4	21.7	22311	4	US-09-949-016-17171	Sequence 17171, A
895	196.6	21.7	152798	4	US-09-949-016-12775	Sequence 12775, A	968	196.4	21.7	22311	4	US-09-949-016-16835	Sequence 16835, A
896	196.6	21.7	152822	4	US-09-949-016-17518	Sequence 17518, A	969	196.4	21.7	22311	4	US-09-949-016-15650	Sequence 15650, A
897	196.6	21.7	152822	4	US-09-949-016-17519	Sequence 17519, A	970	196.4	21.7	22311	4	US-09-949-016-14759	Sequence 14759, A
898	196.6	21.7	784019	4	US-09-949-016-14033	Sequence 14033, A	971	196.4	21.7	32379	4	US-09-949-016-15518	Sequence 15518, A
899	196.6	21.7	828152	4	US-09-949-016-12777	Sequence 12777, A	972	196.4	21.7	32379	4	US-09-949-016-15519	Sequence 15519, A
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901	196.4	21.7	601	4	US-09-949-016-115417	Sequence 115417, A	974	196.4	21.7	32379	4	US-09-949-016-15521	Sequence 15521, A
902	196.4	21.7	601	4	US-09-949-016-136815	Sequence 136815, A	975	196.4	21.7	32379	4	US-09-949-016-15522	Sequence 15522, A
903	196.4	21.7	601	4	US-09-949-016-163105	Sequence 163105, A	976	196.4	21.7	32379	4	US-09-949-016-15523	Sequence 15523, A

977	196.2	21.6	32379	4	US-09-949-016-15224	Sequence 15524, A	C1050	195.8	21.6	601	4	US-09-949-016-114519	Sequence 114519, A
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979	196.2	21.6	32379	4	US-09-949-016-15226	Sequence 15526, A	C1052	195.8	21.6	601	4	US-09-949-016-114655	Sequence 114655, A
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981	196.2	21.6	64377	4	US-09-949-016-15512	Sequence 15512, A	C1054	195.8	21.6	601	4	US-09-949-016-112294	Sequence 112294, A
982	196.2	21.6	64377	4	US-09-949-016-15213	Sequence 15213, A	C1055	195.8	21.6	601	4	US-09-949-016-123048	Sequence 123048, A
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C 987	196.2	21.6	78125	4	US-09-949-016-15006	Sequence 15006, A	C1060	195.8	21.6	601	4	US-09-949-016-123456	Sequence 123456, A
C 988	196.2	21.6	80355	4	US-09-949-016-15375	Sequence 15375, A	C1061	195.8	21.6	601	4	US-09-949-016-123498	Sequence 123498, A
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C 990	196.2	21.6	83617	4	US-09-949-016-14461	Sequence 14461, A	C1063	195.8	21.6	601	4	US-09-949-016-123582	Sequence 123582, A
C 991	196.2	21.6	87870	4	US-09-949-016-14514	Sequence 14514, A	C1064	195.8	21.6	601	4	US-09-949-016-138596	Sequence 138596, A
C 992	196.2	21.6	121970	4	US-09-949-016-17216	Sequence 17216, A	C1065	195.8	21.6	601	4	US-09-949-016-123624	Sequence 123624, A
C 993	196.2	21.6	134140	4	US-09-949-016-15272	Sequence 15272, A	C1066	195.8	21.6	601	4	US-09-949-016-123666	Sequence 123666, A
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997	196.2	21.6	134342	4	US-09-949-016-15815	Sequence 15815, A	C1070	195.8	21.6	601	4	US-09-949-016-175569	Sequence 175569, A
C 998	196.2	21.6	275110	4	US-09-949-016-15206	Sequence 15206, A	C1071	195.8	21.6	601	4	US-09-949-016-195412	Sequence 195412, A
C 999	196.2	21.6	275110	4	US-09-949-016-15070	Sequence 15070, A	C1072	195.8	21.6	3172	3	US-08-978-289-7	Sequence 7, Appl1
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c1125	195.6	21.6	601	4	US-09-949-016-165010	Sequence 165010,
c1126	195.6	21.6	601	4	US-09-949-016-165019	Sequence 165019,
c1127	195.6	21.6	601	4	US-09-949-016-172869	Sequence 172869,
c1128	195.6	21.6	601	4	US-09-949-016-172887	Sequence 172887,
c1129	195.6	21.6	601	4	US-09-949-016-177642	Sequence 177642,
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c1132	195.6	21.6	24214	4	US-09-949-016-13533	Sequence 15511, A
c1133	195.6	21.6	30032	4	US-09-949-016-13933	Sequence 13933, A
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c1135	195.6	21.6	36618	4	US-09-949-016-12861	Sequence 12861, A
c1136	195.6	21.6	38702	4	US-09-949-016-13788	Sequence 13788, A
c1137	195.6	21.6	50217	4	US-09-949-016-16067	Sequence 16067, A
c1138	195.6	21.6	60304	4	US-09-949-016-12218	Sequence 12218, A
c1139	195.6	21.6	60305	4	US-09-949-016-15791	Sequence 15791, A
c1140	195.6	21.6	68719	4	US-09-949-016-12799	Sequence 12799, A
c1141	195.6	21.6	68720	4	US-09-949-016-14296	Sequence 14296, A
c1142	195.6	21.6	98701	4	US-09-949-016-15898	Sequence 15898, A
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c1144	195.6	21.6	129380	4	US-09-949-016-12544	Sequence 12544, A
c1145	195.6	21.6	135010	4	US-09-949-016-17234	Sequence 17234, A
c1146	195.6	21.6	231129	4	US-09-949-016-16110	Sequence 16110, A
c1147	195.6	21.6	266293	4	US-09-949-016-11934	Sequence 11934, A
c1148	195.6	21.6	387902	4	US-09-949-016-14543	Sequence 14543, A
c1149	195.6	21.6	421883	4	US-09-949-016-12557	Sequence 12557, A
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c1152	195.4	21.5	601	4	US-09-949-016-185173	Sequence 185173,
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c1155	195.4	21.5	10103	4	US-09-949-016-15718	Sequence 13245, A
c1156	195.4	21.5	11338	4	US-09-949-016-16583	Sequence 16583, A
c1157	195.4	21.5	13883	4	US-09-949-016-15718	Sequence 15718, A
c1158	195.4	21.5	18157	4	US-09-949-016-16193	Sequence 16193, A
c1159	195.4	21.5	20099	4	US-09-949-016-13074	Sequence 13074, A
c1160	195.4	21.5	23051	4	US-09-949-016-16922	Sequence 16922, A
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c1162	195.4	21.5	32211	4	US-09-949-016-16307	Sequence 16307, A
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c1165	195.4	21.5	49848	4	US-09-949-016-15675	Sequence 15675, A
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c1171	195.4	21.5	6736	4	US-09-949-016-16519	Sequence 16519, A
c1172	195.4	21.5	67620	4	US-09-949-016-16939	Sequence 16939, A
c1173	195.4	21.5	76472	4	US-09-949-016-15896	Sequence 15896, A
c1174	195.4	21.5	76610	4	US-09-949-016-15521	Sequence 15521, A
c1175	195.4	21.5	92276	4	US-09-949-016-12166	Sequence 12166, A
c1176	195.4	21.5	102008	4	US-09-949-016-16617	Sequence 16617, A
c1177	195.4	21.5	116532	4	US-09-818-512-3	Sequence 3, Appl1
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c1180	195.4	21.5	150597	4	US-09-949-016-15379	Sequence 15379, A
c1181	195.4	21.5	258449	4	US-09-949-016-17244	Sequence 17244, A
c1182	195.4	21.5	455726	4	US-09-949-016-14157	Sequence 14157, A
c1183	195.4	21.5	481115	4	US-09-949-016-11940	Sequence 11940, A
c1184	195.4	21.5	818128	4	US-09-949-016-14516	Sequence 14546, A
c1185	195.4	21.5	818128	4	US-09-949-016-14547	Sequence 14547, A
c1186	195.4	21.5	818128	4	US-09-949-016-14548	Sequence 14548, A
c1187	195.4	21.5	818128	4	US-09-949-016-14549	Sequence 14549, A
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c1190	195.4	21.5	818128	4	US-09-949-016-14552	Sequence 14552, A
c1191	195.4	21.5	818128	4	US-09-949-016-14553	Sequence 14553, A
c1192	195.4	21.5	818128	4	US-09-949-016-14554	Sequence 14554, A
c1193	195.4	21.5	818128	4	US-09-949-016-14555	Sequence 14555, A
c1194	195.4	21.5	818128	4	US-09-949-016-14556	Sequence 14556, A
c1195	195.4	21.5	818128	4	US-09-949-016-14557	Sequence 14557, A
c1196	195.4	21.5	818128	4	US-09-949-016-14558	Sequence 14558, A
c1197	195.4	21.5	818128	4	US-09-949-016-14559	Sequence 14559, A
c1198	195.4	21.5	818128	4	US-09-949-016-14560	Sequence 14560, A
c1199	195.4	21.5	818128	4	US-09-949-016-14561	Sequence 14561, A
c1200	195.4	21.5	818128	4	US-09-949-016-14562	Sequence 14562, A
c1201	195.4	21.5	818128	4	US-09-949-016-14563	Sequence 14563, A
c1202	195.4	21.5	818128	4	US-09-949-016-14564	Sequence 14564, A
c1203	195.4	21.5	818128	4	US-09-949-016-14565	Sequence 14565, A
c1204	195.4	21.5	818128	4	US-09-949-016-14566	Sequence 14566, A
c1205	195.4	21.5	818128	4	US-09-949-016-14567	Sequence 14567, A
c1206	195.2	21.5	601	4	US-09-949-016-12580	Sequence 29580, A
c1207	195.2	21.5	601	4	US-09-949-016-63625	Sequence 69625, A
c1208	195.2	21.5	601	4	US-09-949-016-63625	Sequence 69625, A
c1209	195.2	21.5	601	4	US-09-949-016-148057	Sequence 75729, A
c1210	195.2	21.5	601	4	US-09-949-016-148057	Sequence 148057, A
c1211	195.2	21.5	6647	4	US-09-949-016-19138	Sequence 19138, A
c1212	195.2	21.5	11729	4	US-09-949-016-16079	Sequence 16079, A
c1213	195.2	21.5	25111	4	US-09-949-016-13247	Sequence 13247, A
c1214	195.2	21.5	25111	4	US-09-949-016-14345	Sequence 12435, A
c1215	195.2	21.5	25111	4	US-09-949-016-13944	Sequence 13944, A
c1216	195.2	21.5	27270	4	US-09-949-016-11822	Sequence 13822, A
c1217	195.2	21.5	27923	4	US-09-949-016-15390	Sequence 15390, A
c1218	195.2	21.5	28393	4	US-09-949-016-13771	Sequence 13771, A
c1219	195.2	21.5	31318	4	US-09-949-016-16880	Sequence 16980, A
c1220	195.2	21.5	31319	4	US-09-949-016-12495	Sequence 12495, A
c1221	195.2	21.5	3268	4	US-09-949-016-15963	Sequence 15963, A
c1222	195.2	21.5	33661	4	US-09-949-016-17406	Sequence 17406, A
c1223	195.2	21.5	33661	3	US-08-814-095-7	Sequence 16848, A
c1224	195.2	21.5	48018	4	US-09-949-016-17573	Sequence 7, Appl1
c1225	195.2	21.5	48018	4	US-09-949-016-15555	Sequence 17555, A
c1226	195.2	21.5	48108	4	US-09-949-016-15955	Sequence 12555, A
c1227	195.2	21.5	48763	4	US-09-949-016-16942	Sequence 16942, A
c1228	195.2	21.5	48763	4	US-09-916-204-3	Sequence 3, Appl1
c1229	195.2	21.5	70014	4	US-10-282-048-3	Sequence 3, Appl1
c1230	195.2	21.5	84252	4	US-09-949-016-17110	Sequence 17110, A
c1231	195.2	21.5	113042	4	US-09-949-016-17315	Sequence 17315, A
c1232	195.2	21.5	113042	4	US-09-949-016-12443	Sequence 12343, A
c1233	195.2	21.5	144158	4	US-09-949-016-15246	Sequence 15246, A
c1234	195.2	21.5	144158	4	US-09-949-016-11755	Sequence 11755, A
c1235	195.2	21.5	150409	4	US-09-949-016-12936	Sequence 12936, A
c1236	195.2	21.5	150409	4	US-09-949-016-12936	Sequence 12936, A
c1237	195.2	21.5	326820	4	US-09-949-016-14139	Sequence 14139, A
c1238	195.2	21.5	45095	4	US-09-949-016-15473	Sequence 15473, A
c1239	195.2	21.5	601	4	US-09-949-016-23901	Sequence 23901, A
c1240	195.2	21.5	601	4	US-09-949-016-46249	Sequence 46249, A
c1241	195.2	21.5	601	4	US-09-949-016-89146	Sequence 89146, A
c1242	195.2	21.5	601	4	US-09-949-016-141104	Sequence 141104, A
c1243	195.2	21.5	601	4	US-09-949-016-165186	Sequence 165186, A
c1244	195.2	21.5	601	4	US-09-949-016-165298	Sequence 165298, A
c1245	195.2	21.5	601	4	US-09-949-016-165266	Sequence 165266, A
c1246	195.2	21.5	8095	4	US-09-949-016-12307	Sequence 12307, A
c1247	195.2	21.5	8096	4	US-09-949-016-16214	Sequence 16214, A
c1248	195.2	21.5	9740	4	US-09-949-016-15916	Sequence 15916, A
c1249	195.2	21.5	10503	4	US-09-949-016-15916	Sequence 15916, A
c1250	195.2	21.5	17377	4	US-09-949-016-16314	Sequence 16314, A
c1251	195.2	21.5	23334	4	US-09-949-016-17331	Sequence 17331, A
c1252	195.2	21.5	26887	4	US-09-949-016-16332	Sequence 16332, A
c1253	195.2	21.5	26887	4	US-09-949-016-16332	Sequence 16332, A
c1254	195.2	21.5	29321	4	US-09-949-016-14257	Sequence 14257, A
c1255	195.2	21.5	29321	4	US-09-949-016-14257	Sequence 14257, A
c1256	195.2	21.5	29927	4	US-09-949-016-14558	Sequence 14558, A
c1257	195.2	21.5	29927	4	US-09-949-016-15885	Sequence 15885, A
c1258	195.2	21.5	29927	4	US-09-949-016-15885	Sequence 15885, A
c1259	195.2	21.5	30418	4	US-09-949-016-12347	Sequence 12347, A
c1260	195.2	21.5	30418	4	US-09-949-016-14759	Sequence 14759, A
c1261	195.2	21.5	31618	4	US-09-949-016-12639	Sequence 12639, A
c1262	195.2	21.5	40130	4	US-09-949-016-17775	Sequence 17775, A
c1263	195.2	21.5	40130	4	US-09-949-016-17775	Sequence 17775, A
c1264	195.2	21.5	47979	4	US-09-949-016-13563	Sequence 13563, A
c1265	195.2	21.5	49848	4	US-09-949-016-15675	Sequence 15675, A
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1270	195	21.5	61124	4	US-09-949-016-11914	Sequence 11914, A	1343	194.6	21.5	601	4	US-09-949-016-184699	Sequence 184699,
1271	195	21.5	61140	4	US-09-949-016-15771	Sequence 15771, A	1344	194.6	21.5	601	4	US-09-949-016-193121	Sequence 193121,
1272	195	21.5	66219	4	US-09-949-016-12038	Sequence 12038, A	1345	194.6	21.5	601	4	US-09-949-016-193214	Sequence 193214,
c1273	195	21.5	66219	4	US-09-949-016-12038	Sequence 12038, A	1346	194.6	21.5	601	4	US-09-949-016-193307	Sequence 193307,
1274	195	21.5	66227	4	US-09-949-016-15303	Sequence 15303, A	1347	194.6	21.5	601	4	US-09-949-016-193400	Sequence 193400,
c1275	195	21.5	66227	4	US-09-949-016-15303	Sequence 15303, A	1348	194.6	21.5	10148	4	US-09-949-016-13252	Sequence 13252, A
1276	195	21.5	75395	4	US-09-984-890-3	Sequence 3, App1	c1349	194.6	21.5	15363	4	US-09-949-016-13571	Sequence 13571, A
1277	195	21.5	75395	4	US-10-274-194-3	Sequence 3, App1	1350	194.6	21.5	15363	4	US-09-949-016-18298	Sequence 18298, A
c1279	195	21.5	82000	4	US-09-949-016-15595	Sequence 15595, A	1351	194.6	21.5	17328	4	US-09-949-016-15736	Sequence 15736, A
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1281	195	21.5	86213	4	US-09-949-016-17240	Sequence 17240, A	c1353	194.6	21.5	27412	4	US-09-949-016-17025	Sequence 17025, A
1282	195	21.5	86213	4	US-09-949-016-17241	Sequence 17241, A	1354	194.6	21.5	28109	4	US-09-949-016-13329	Sequence 13329, A
1283	195	21.5	86213	4	US-09-949-016-17242	Sequence 17242, A	c1355	194.6	21.5	41684	4	US-09-536-059-1	Sequence 1, App1
1284	195	21.5	86213	4	US-09-949-016-17243	Sequence 17243, A	c1356	194.6	21.5	43576	4	US-09-949-016-13364	Sequence 13364, A
c1285	195	21.5	100877	4	US-09-949-016-13776	Sequence 13276, A	c1357	194.6	21.5	43377	4	US-09-949-016-118183	Sequence 12183, A
c1286	195	21.5	123863	4	US-09-949-016-14353	Sequence 13453, A	c1358	194.6	21.5	49440	4	US-09-949-016-11598	Sequence 14150, A
1287	195	21.5	123863	4	US-09-949-016-14353	Sequence 14353, A	1359	194.6	21.5	50269	4	US-09-949-016-15440	Sequence 17598, A
c1288	194.8	21.5	601	4	US-09-949-016-70399	Sequence 70399, A	c1360	194.6	21.5	57507	4	US-09-949-016-15019	Sequence 15019, A
1289	194.8	21.5	601	4	US-09-949-016-121140	Sequence 121140, A	c1361	194.6	21.5	69701	4	US-09-949-016-14187	Sequence 14187, A
1290	194.8	21.5	601	4	US-09-949-016-124427	Sequence 124427, A	1362	194.6	21.5	71245	4	US-09-949-016-12126	Sequence 12326, A
1291	194.8	21.5	601	4	US-09-949-016-180851	Sequence 180851, A	1363	194.6	21.5	71651	4	US-09-949-016-11258	Sequence 17258, A
1292	194.8	21.5	601	4	US-09-949-016-183999	Sequence 183999, A	c1364	194.6	21.5	72662	4	US-09-949-016-17073	Sequence 17073, A
1293	194.8	21.5	601	4	US-09-949-016-184104	Sequence 184104, A	c1365	194.6	21.5	73308	4	US-09-949-016-15326	Sequence 16326, A
c1294	194.8	21.5	601	4	US-09-949-016-184209	Sequence 184209, A	c1366	194.6	21.5	99304	4	US-09-949-016-15440	Sequence 15440, A
1295	194.8	21.5	601	4	US-09-949-016-184314	Sequence 184314, A	1367	194.6	21.5	120727	4	US-09-949-016-15787	Sequence 15787, A
c1296	194.8	21.5	601	4	US-09-949-016-189485	Sequence 189485, A	c1368	194.6	21.5	120727	4	US-09-949-016-15788	Sequence 15788, A
c1297	194.8	21.5	11380	4	US-09-949-016-17172	Sequence 17172, A	c1369	194.6	21.5	132438	4	US-09-949-016-13349	Sequence 14339, A
c1298	194.8	21.5	25769	4	US-09-949-016-17154	Sequence 17154, A	c1370	194.6	21.5	133253	4	US-09-949-016-14350	Sequence 14350, A
c1299	194.8	21.5	29453	4	US-09-949-016-129330	Sequence 129330, A	c1371	194.6	21.5	137758	4	US-09-949-016-114054	Sequence 17404, A
c1300	194.8	21.5	29453	4	US-09-949-016-129340	Sequence 129340, A	c1372	194.6	21.5	147440	4	US-09-949-016-15236	Sequence 15236, A
c1301	194.8	21.5	29453	4	US-09-949-016-12941	Sequence 12941, A	c1373	194.6	21.5	151089	4	US-09-949-016-13348	Sequence 14348, A
c1302	194.8	21.5	29453	4	US-09-949-016-12942	Sequence 12942, A	c1374	194.6	21.5	524032	4	US-09-949-016-16928	Sequence 16928, A
c1303	194.8	21.5	31602	4	US-09-949-016-16561	Sequence 16561, A	c1375	194.6	21.5	524032	4	US-09-949-016-16928	Sequence 16928, A
c1304	194.8	21.5	36759	4	US-09-949-016-12216	Sequence 12216, A	1376	194.6	21.5	524032	4	US-09-949-016-15929	Sequence 16929, A
c1305	194.8	21.5	36759	4	US-09-949-016-12216	Sequence 12216, A	c1377	194.6	21.5	524032	4	US-09-949-016-16929	Sequence 16929, A
c1306	194.8	21.5	38346	4	US-09-949-016-14502	Sequence 14502, A	c1378	194.6	21.5	524032	4	US-09-949-016-16930	Sequence 16930, A
c1307	194.8	21.5	39754	4	US-09-949-016-14502	Sequence 14502, A	c1379	194.6	21.5	524032	4	US-09-949-016-16931	Sequence 16931, A
c1308	194.8	21.5	41380	4	US-09-949-016-15128	Sequence 15128, A	c1381	194.6	21.5	524032	4	US-09-949-016-15931	Sequence 16931, A
1309	194.8	21.5	42235	4	US-09-949-016-12558	Sequence 12558, A	1382	194.6	21.5	529885	4	US-09-949-016-13340	Sequence 14340, A
c1310	194.8	21.5	42235	4	US-09-949-016-12558	Sequence 12558, A	c1383	194.6	21.5	529885	4	US-09-949-016-13340	Sequence 14340, A
c1311	194.8	21.5	48682	4	US-09-949-016-17237	Sequence 17237, A	c1384	194.6	21.5	529885	4	US-09-949-016-13341	Sequence 14341, A
c1312	194.8	21.5	48682	4	US-09-949-016-17238	Sequence 17238, A	c1385	194.6	21.5	529885	4	US-09-949-016-13342	Sequence 14342, A
c1313	194.8	21.5	48682	4	US-09-949-016-17239	Sequence 17239, A	1386	194.6	21.5	529885	4	US-09-949-016-13342	Sequence 14342, A
c1314	194.8	21.5	51022	4	US-09-949-016-17136	Sequence 17136, A	c1387	194.6	21.5	529885	4	US-09-949-016-13342	Sequence 14342, A
c1315	194.8	21.5	51022	4	US-09-949-016-17136	Sequence 17136, A	1388	194.6	21.5	529885	4	US-09-949-016-13343	Sequence 14343, A
c1316	194.8	21.5	51022	4	US-09-949-016-17137	Sequence 17137, A	c1389	194.6	21.5	529885	4	US-09-949-016-13343	Sequence 14343, A
c1317	194.8	21.5	51022	4	US-09-949-016-17138	Sequence 17138, A	1390	194.6	21.5	529885	4	US-09-949-016-13344	Sequence 14344, A
c1318	194.8	21.5	69752	4	US-09-949-016-14094	Sequence 14094, A	c1391	194.6	21.5	529885	4	US-09-949-016-13344	Sequence 14344, A
1319	194.8	21.5	75226	4	US-09-949-016-14061	Sequence 14061, A	1392	194.6	21.5	529885	4	US-09-949-016-13345	Sequence 14345, A
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c1321	194.8	21.5	78720	4	US-09-949-016-12710	Sequence 12710, A	c1394	194.6	21.5	529885	4	US-09-949-016-13346	Sequence 14346, A
c1322	194.8	21.5	86213	4	US-09-949-016-17240	Sequence 17240, A	c1395	194.6	21.5	529885	4	US-09-949-016-13346	Sequence 14346, A
c1323	194.8	21.5	86213	4	US-09-949-016-17241	Sequence 17241, A	c1396	194.6	21.5	529885	4	US-09-949-016-13347	Sequence 14347, A
c1324	194.8	21.5	86213	4	US-09-949-016-17242	Sequence 17242, A	c1397	194.6	21.5	529885	4	US-09-949-016-13347	Sequence 14347, A
c1325	194.8	21.5	86213	4	US-09-949-016-17243	Sequence 17243, A	1398	194.4	21.4	601	4	US-09-949-016-18151	Sequence 18151, A
1326	194.8	21.5	86300	4	US-09-949-016-14837	Sequence 14837, A	c1399	194.4	21.4	601	4	US-09-949-016-18629	Sequence 80629, A
c1328	194.8	21.5	87039	4	US-09-949-016-15691	Sequence 15691, A	1400	194.4	21.4	601	4	US-09-949-016-186810	Sequence 105810, A
c1329	194.8	21.5	96987	4	US-09-949-016-14429	Sequence 14429, A	c1401	194.4	21.4	601	4	US-09-949-016-186877	Sequence 108477, A
c1330	194.8	21.5	96987	4	US-09-949-016-14429	Sequence 14429, A	c1402	194.4	21.4	601	4	US-09-949-016-186877	Sequence 108477, A
1331	194.8	21.5	112112	4	US-09-949-016-15639	Sequence 15639, A	1403	194.4	21.4	601	4	US-09-949-016-112381	Sequence 112381, A
1332	194.8	21.5	112112	4	US-09-949-016-15639	Sequence 15639, A	1404	194.4	21.4	601	4	US-09-949-016-126869	Sequence 162869, A
1333	194.8	21.5	144596	4	US-09-949-016-11749	Sequence 11749, A	c1405	194.4	21.4	601	4	US-09-949-016-189757	Sequence 189757, A
c1334	194.8	21.5	144596	4	US-09-949-016-11749	Sequence 11749, A	c1406	194.4	21.4	601	4	US-09-949-016-201582	Sequence 201582, A
c1335	194.8	21.5	178883	4	US-09-949-016-12733	Sequence 12733, A	1407	194.4	21.4	7070	4	US-09-949-016-13322	Sequence 13322, A
c1336	194.8	21.5	178883	4	US-09-949-016-12733	Sequence 12733, A	c1408	194.4	21.4	7070	4	US-09-949-016-13322	Sequence 13322, A
c1337	194.8	21.5	250352	4	US-09-949-016-14724	Sequence 14724, A	c1409	194.4	21.4	8150	4	US-09-949-016-13830	Sequence 13830, A
1338	194.8	21.5	390880	4	US-09-949-016-14720	Sequence 14720, A	1410	194.4	21.4	15927	4	US-09-949-016-12228	Sequence 12228, A
c1339	194.6	21.5	304	4	US-09-513-9996-25334	Sequence 25334, A	1411	194.4	21.4	18725	4	US-09-949-016-13977	Sequence 15977, A
c1340	194.6	21.5	601	4	US-09-949-016-51220	Sequence 51220, A	1412	194.4	21.4	34534	4	US-09-949-016-15141	Sequence 15141, A
1341	194.6	21.5	601	4	US-09-949-016-118217	Sequence 118217, A	1413	194.4	21.4	35104	4	US-09-949-016-15831	Sequence 15831, A
					US-09-949-016-154652	Sequence 154652, A	c1414	194.4	21.4	37711	4	US-09-949-016-182832	Sequence 12832, A

C1415	194.4	21.4	37712	4	US-09-949-016-16704	Sequence 16704, A
C1416	194.4	21.4	50368	4	US-09-949-016-13356	Sequence 13256, A
C1417	194.4	21.4	54346	4	US-09-949-016-16206	Sequence 16206, A
C1418	194.4	21.4	63760	4	US-09-949-016-14087	Sequence 14087, A
C1419	194.4	21.4	75312	4	US-09-949-016-14088	Sequence 14088, A
C1420	194.4	21.4	75312	4	US-09-949-016-13313	Sequence 13313, A
C1421	194.4	21.4	75312	4	US-09-949-016-13314	Sequence 13314, A
C1422	194.4	21.4	75312	4	US-09-949-016-13315	Sequence 13315, A
C1423	194.4	21.4	83462	4	US-09-949-016-15116	Sequence 15116, A
C1424	194.4	21.4	84916	4	US-09-949-016-14736	Sequence 14736, A
C1425	194.4	21.4	87523	4	US-09-949-016-12670	Sequence 12670, A
C1426	194.4	21.4	87523	4	US-09-949-016-15047	Sequence 15047, A
C1427	194.4	21.4	87523	4	US-09-949-016-15048	Sequence 15048, A
C1428	194.4	21.4	87523	4	US-09-949-016-15049	Sequence 15049, A
C1429	194.4	21.4	87869	4	US-09-949-016-11744	Sequence 11744, A
C1430	194.4	21.4	87869	4	US-09-949-016-15044	Sequence 15044, A
C1431	194.4	21.4	87869	4	US-09-949-016-15045	Sequence 15045, A
C1432	194.4	21.4	87869	4	US-09-949-016-15046	Sequence 15046, A
C1433	194.4	21.4	100836	4	US-09-949-016-12871	Sequence 12871, A
C1434	194.4	21.4	100837	4	US-09-949-016-17063	Sequence 17063, A
C1435	194.4	21.4	118136	4	US-09-949-016-12439	Sequence 12439, A
C1436	194.4	21.4	194937	4	US-09-949-016-17032	Sequence 17032, A
C1437	194.4	21.4	228851	4	US-09-949-016-17033	Sequence 17033, A
C1438	194.4	21.4	228851	4	US-09-949-016-13781	Sequence 13781, A
C1439	194.4	21.4	260247	4	US-09-949-016-13358	Sequence 13358, A
C1440	194.4	21.4	283	4	US-08-579-445-26	Sequence 26, Appl
C1441	194.2	21.4	601	4	US-09-949-016-58582	Sequence 58582, A
C1442	194.2	21.4	601	4	US-09-949-016-60226	Sequence 60226, A
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C1444	194.2	21.4	601	4	US-09-949-016-96520	Sequence 96520, A
C1445	194.2	21.4	601	4	US-09-949-016-96786	Sequence 96786, A
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C1447	194.2	21.4	601	4	US-09-949-016-97318	Sequence 97318, A
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C1450	194.2	21.4	601	4	US-09-949-016-98116	Sequence 98116, A
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C1452	194.2	21.4	601	4	US-09-949-016-98648	Sequence 98648, A
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C1460	194.2	21.4	601	4	US-09-949-016-100776	Sequence 100776, A
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C1462	194.2	21.4	601	4	US-09-949-016-101346	Sequence 101346, A
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C1469	194.2	21.4	601	4	US-09-949-016-143344	Sequence 143344, A
C1470	194.2	21.4	601	4	US-09-949-016-143515	Sequence 143515, A
C1471	194.2	21.4	601	4	US-09-949-016-154653	Sequence 154653, A
C1472	194.2	21.4	601	4	US-09-949-016-160006	Sequence 160006, A
C1473	194.2	21.4	4428	4	US-09-023-655-1109	Sequence 1109, App
C1474	194.2	21.4	8165	4	US-09-949-016-16816	Sequence 16816, A
C1475	194.2	21.4	9157	4	US-09-949-016-16185	Sequence 16185, A
C1476	194.2	21.4	14961	4	US-09-949-016-13400	Sequence 13400, A
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C1478	194.2	21.4	20674	3	US-09-641-638-651	Sequence 651, App
C1479	194.2	21.4	20674	4	US-10-170-097-651	Sequence 651, App
C1480	194.2	21.4	35688	4	US-09-949-016-16873	Sequence 16873, A
C1481	194.2	21.4	37269	4	US-09-949-016-16672	Sequence 16672, A
C1482	194.2	21.4	41613	4	US-09-949-016-16125	Sequence 16125, A
C1483	194.2	21.4	43657	4	US-09-949-016-13777	Sequence 13777, A
C1484	194.2	21.4	57875	4	US-09-949-016-13152	Sequence 13152, A
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C1487	194.2	21.4	84425	4	US-09-949-016-17402	Sequence 17402, A

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1490 194.2 21.4 151088 4 US-09-949-016-16240 Sequence 16240, A
1491 194.2 21.4 160759 4 US-09-949-016-16514 Sequence 16514, A
1492 194.2 21.4 177293 4 US-09-949-016-16513 Sequence 16513, A
C1493 194.2 21.4 197131 4 US-09-949-016-16753 Sequence 16753, A
C1494 194.2 21.4 197132 4 US-09-949-016-17170 Sequence 17170, A
C1495 194.2 21.4 227392 4 US-09-949-016-12201 Sequence 12201, A
C1496 194.2 21.4 227391 4 US-09-949-016-13365 Sequence 13365, A
C1497 194.2 21.4 251672 4 US-09-949-016-11296 Sequence 11296, A
1498 194.2 21.4 251682 4 US-09-949-016-11973 Sequence 11973, A
C1499 194 21.4 601 4 US-09-949-016-17631 Sequence 17631, A
C1500 194 21.4 601 4 US-09-949-016-24001 Sequence 24001, A

ALIGNMENTS

RESULT 1
US-09-949-016-14632
; Sequence 14632, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14632
; LENGTH: 12445
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(12445)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14632

Query Match 99.9%; Score 905.4; DB 4; Length 12445;
Best Local Similarity 99.9%; Pred. No. 1.7e-271;
Matches 906; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB GAGCTTGAGAGGCCAGACAGCTGCTGAGGCCGCCAGAGAGTGGTTCCAGCTTGGAC 11241
QY 61 CCTTAGGGTCTGAGATTGCTGTTAAAGATTAACCTTAGGGCAGACCCATAGGGGA 120
DB CCTTAGGGTCTGAGATTGCTGTTAAAGATTAACCTTAGGGCAGACCCATAGGGGA 11241
QY 11242 CCTTAGGGTCTGAGATTGCTGTTAAAGATTAACCTTAGGGCAGACCCATAGGGGA 11301
DB CCTTAGGGTCTGAGATTGCTGTTAAAGATTAACCTTAGGGCAGACCCATAGGGGA 11301
QY 121 ATGCTACTCTCCGACCTTCACTGCTGATTCACGATGGCTGTCTCTTGGCC 180
DB ATGCTACTCTCCGACCTTCACTGCTGATTCACGATGGCTGTCTCTTGGCC 11361
QY 11302 ATGCTACTCTCCGACCTTCACTGCTGATTCACGATGGCTGTCTCTTGGCC 11361
DB ATGCTACTCTCCGACCTTCACTGCTGATTCACGATGGCTGTCTCTTGGCC 11361
QY 181 GAGAGAGTCTCTGGGTGACGAGGACGAGAGAGCTCAAGACTCAAGCCCTTGTACC 240
DB GAGAGAGTCTCTGGGTGACGAGGACGAGAGAGCTCAAGACTCAAGCCCTTGTACC 11421
QY 241 GAGAGAGCACTTGGCAAGTCCAGCGATGTCGGAGTCCACACAGATGGCGGACG 300
DB GAGAGAGCACTTGGCAAGTCCAGCGATGTCGGAGTCCACACAGATGGCGGACG 11481
QY 11422 GAGAGAGCACTTGGCAAGTCCAGCGATGTCGGAGTCCACACAGATGGCGGACG 11481
DB GAGAGAGCACTTGGCAAGTCCAGCGATGTCGGAGTCCACACAGATGGCGGACG 11481
QY 301 GAGAGAGGGGAGCAGTTCTGTGCTGCTTGGATGAGCAGTAAAGGCTTGGCAGTCA 360
DB GAGAGAGGGGAGCAGTTCTGTGCTGCTTGGATGAGCAGTAAAGGCTTGGCAGTCA 360

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Db      11482 GCAGGAGGGGGGACAGTCTGTGTGTGTGTGTGAACAAGTAAGGGGTCTTGCCCAATGCCA 11541
QY      GGGTGGGGGGCGCGCAAATTCCATAAAGAACCAGAGGGGTCTGGCCCCCGGCACAGAGTCA 420
Db      11542 GGGTGGGGGGCGCGCAAATTCCATAAAGAACCAGAGGGGTCTGGCCCCCGGCACAGAGTCA 11601
QY      TCTGCGCAGCTCTCTGCTGCTGCGCCAGTGGGAGTAGTGGCACAGAGTGGGGCTTTGTGCCAG 480
Db      11602 TCTGCGCAGCTCTCTGCTGCTGCGCCAGTGGGAGTAGTGGCACAGAGTGGGGCTTTGTGCCAG 11661
QY      TAAACCAACAGGCTGGATTTCCTGCGGGCCAGTGTCCCTGTCTTAGGGGACGAATTTCTCA 540
Db      11662 TAAACCAACAGGCTGGATTTCCTGCGGGCCAGTGTCCCTGTCTTAGGGGACGAATTTCTCA 11721
QY      ACCCTCTTGCTCTCAGAACCCCAAGAGCTTTTCATTGTATCTATGATTTTTCACACTT 600
Db      11722 ACCCTCTTGCTCTCAGAACCCCAAGAGCTTTTCATTGTATCTATGATTTTTCACACTT 11781
QY      AGCATTTAAACTGAGAAATGGGGCCGGGACAGGTGGCTACACGCTGTAAATCCAGACTT 660
Db      11782 AGCATTTAAACTGAGAAATGGGGCCGGGACAGGTGGCTACACGCTGTAAATCCAGACTT 11841
QY      TGGAGAGCCGAGGCGGGGTGATTCACCTGAGATCAGAGATTCAAGACCAAGCTGGCCACA 720
Db      11842 TGGAGAGCCGAGGCGGGGTGATTCACCTGAGATCAGAGATTCAAGACCAAGCTGGCCACA 11901
QY      TGGTAAACCTTGTCTACTTAAATAATACAAAATAATTAGCCAGACCAAGTGGTGTGCAC 780
Db      11902 TGGTAAACCTTGTCTACTTAAATAATACAAAATAATTAGCCAGGACCAAGTGGTGTGCAC 11961
QY      TAGTCCCAGTTACTCTGGGAGGCGTGGAGGCGAGAAATTCGCTGAAACCAGAGGCGGACGT 840
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QY      901 TCACACA 907
Db      12082 TCACACA 12088

RESULT 2
US-09-949-016-15748
; Sequence 15748, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001037
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 15748
; LENGTH: 21691
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(21691)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15748
Query Match          99.8%; Score 905.4; DB 4; Length 21691;
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[illegible]

Query Match 23.1%; Score 209.2; DB 4; Length 35678;
Best Local Similarity 79.7%; Pred. No. 4e-54;
Matches 247; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 598 ATTGACATTTAAACTGAGAAATGGCGCGGCGGCGCTGACGCTGTAATCCCGACA 657
DB 10261 ATATGATTTAAATAATATAGAGACGCTGGCACAGTGCTTATGCTTATATCCCGACA 10202

QY 658 CTTTGGAGGCCGAGCGGGGTGATCACTGAGATCAGAGTTCAAGACCAAGCCTGGCCA 717
DB 10201 CTTTGGAGGCCGAGCGGGGTGATCACTGAGATCAGAGTTCAAGACCAAGCCTGGCCA 10142

QY 718 ACATGCTGAACCTTGTCTACTATAAAATACAAAAATTAGCCAGGCAAGTGTGTGCAC 777
DB 10141 ACATGCTGAACCTTGTCTACTATAAAATACAAAAATTAGCCAGGCAAGTGTGTGCAC 10082

QY 778 TGGTAGTCCCACTTACTCTGGGAGGCTGAGGCAAGAAAAATCGTTGAACCCAGAGGCGGA 837
DB 10081 CTATTAATCCAGCTACTCGGAGGCTGAGGCAAGAAATCACTGGAACCCAGAGGAGTGA 10022

QY 898 ATCTCACACA 907
DB 9961 GTCTCAAAAA 9952

RESULT 13
US-09-949-016-16757/c
; Sequence 16757, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16757
; LENGTH: 35678
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16757

Query Match 23.1%; Score 209.2; DB 4; Length 35678;
Best Local Similarity 79.7%; Pred. No. 4e-54;
Matches 247; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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DB 10261 ATATGATTTAAATAATATAGAGACGCTGGCACAGTGCTTATGCTTATATCCCGACA 10202

QY 658 CTTTGGAGGCCGAGCGGGGTGATCACTGAGATCAGAGTTCAAGACCAAGCCTGGCCA 717
DB 10201 CTTTGGAGGCCGAGCGGGGTGATCACTGAGATCAGAGTTCAAGACCAAGCCTGGCCA 10142

QY 718 ACATGCTGAACCTTGTCTACTATAAAATACAAAAATTAGCCAGGCAAGTGTGTGCAC 777
DB 10141 ACATGCTGAACCTTGTCTACTATAAAATACAAAAATTAGCCAGGCAAGTGTGTGCAC 10082

QY 778 TGGTAGTCCCACTTACTCTGGGAGGCTGAGGCAAGAAAAATCGTTGAACCCAGAGGCGGA 837
DB 10081 CTATTAATCCAGCTACTCGGAGGCTGAGGCAAGAAATCACTGGAACCCAGAGGAGTGA 10022

QY 898 ATCTCACACA 907
DB 9961 GTCTCAAAAA 9952

QY 838 CGTTGGCGTGAAGCCGAGATCGCGCGGCTGATTCAGCCTGGGCGACAGAGTGAAGTCC 897
DB 10021 GGTTCAGTGAAGTGAAGATCAAGCACTGACCTGAGGCTGAGAGAGTGAAGTCT 9962

QY 898 ATCTCACACA 907
DB 9961 GTCTCAAAAA 9952

RESULT 14
US-09-949-016-16758/c
; Sequence 16758, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16758
; LENGTH: 35678
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16758

Query Match 23.1%; Score 209.2; DB 4; Length 35678;
Best Local Similarity 79.7%; Pred. No. 4e-54;
Matches 247; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

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DB 10261 ATATGATTTAAATAATATAGAGACGCTGGCACAGTGCTTATGCTTATATCCCGACA 10202

QY 658 CTTTGGAGGCCGAGCGGGGTGATCACTGAGATCAGAGTTCAAGACCAAGCCTGGCCA 717
DB 10201 CTTTGGAGGCCGAGCGGGGTGATCACTGAGATCAGAGTTCAAGACCAAGCCTGGCCA 10142

QY 718 ACATGCTGAACCTTGTCTACTATAAAATACAAAAATTAGCCAGGCAAGTGTGTGCAC 777
DB 10141 ACATGCTGAACCTTGTCTACTATAAAATACAAAAATTAGCCAGGCAAGTGTGTGCAC 10082

QY 778 TGGTAGTCCCACTTACTCTGGGAGGCTGAGGCAAGAAAAATCGTTGAACCCAGAGGCGGA 837
DB 10081 CTATTAATCCAGCTACTCGGAGGCTGAGGCAAGAAATCACTGGAACCCAGAGGAGTGA 10022

QY 838 CGTTGGCGTGAAGCCGAGATCGCGCGGCTGATTCAGCCTGGGCGACAGAGTGAAGTCC 897
DB 10021 GGTTCAGTGAAGTGAAGATCAAGCACTGACCTGAGGCTGAGAGAGTGAAGTCT 9962

QY 898 ATCTCACACA 907
DB 9961 GTCTCAAAAA 9952

RESULT 15
US-09-949-016-16755/c
; Sequence 16755, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307

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OM nucleic - nucleic search, using sw model

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Title: US-09-989-733-398

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Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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Listing first 1500 summaries

Database:

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2: gb_esc2:*
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6: gb_esc5:*
7: gb_esc6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 4	469	51.7	470	2	BF912836 IL3-UT011
C 5	466.4	51.4	792	6	CB985553 AGENCOURT
C 6	458	50.5	480	1	AA464988 z280a06.r
C 7	403	44.4	425	1	AA293138 z26e06.r
C 8	369	40.7	402	1	AA393124 zc49a02.r
C 9	344.2	37.9	350	1	AA481356 zV44d03.r
C 10	334.4	36.9	547	4	BM854082 K-EST0135
C 11	308	34.0	511	4	BF963567 PM1-NN120
C 12	308	34.0	511	4	BI034628 PM1-NN120
C 13	304.8	33.6	308	7	CN277578 170006001
C 14	281.4	31.0	363	1	AL133867 DKFZP761H
C 15	271.2	29.9	319	2	BF903767 PM1-MT019
C 16	238.2	26.3	406	1	AV710673 AV710673
C 17	233.4	25.7	510	4	BC995746 MR2-RT116
C 18	231.6	25.5	287	4	BF959092 PM1-NN120
C 19	228.8	25.2	962	2	BF693667 602081854
C 20	222	24.5	1086	4	BM544700 AGENCOURT
C 21	215	23.7	231	2	BF912829 IL3-UT011
C 22	212	23.3	609	6	CB370005 TRFSTY96
C 23	211.2	23.4	480	5	BX483243 DKFZP686G
C 24	210.8	23.2	592	5	BP320355 BP320355

C 25	209.2	23.1	481	6	CA391442
C 26	208.6	23.0	640	8	AZ519506
C 27	208.4	23.0	692	1	AV700758
C 28	208.2	23.0	413	1	AV764406
C 29	207.8	22.9	490	7	H59651
C 30	207.8	22.9	521	8	AQ784619 HS_3248-A
C 31	207.4	22.9	398	5	BK484839
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C 34	206.8	22.8	692	9	AG126921
C 35	206.4	22.8	645	9	AG126921
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C 37	205.8	22.7	274	4	BF957905
C 38	205.8	22.7	558	4	BM66389
C 39	205.8	22.7	584	4	BP301691
C 40	205	22.6	488	1	AA20582
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C 42	205	22.6	1500	3	BC021103
C 43	204.6	22.6	514	8	BS1474
C 44	204.6	22.6	810	4	BP968874
C 45	204.4	22.5	429	7	CN264016
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C 48	204.4	22.5	687	3	BC019875
C 49	204	22.5	402	5	BO631269
C 50	204	22.5	472	5	BU790005
C 51	204	22.5	472	8	AQ310879
C 52	204	22.5	555	8	AQ316808
C 53	204	22.5	690	9	AG088570
C 54	203.8	22.5	392	5	BQ271642
C 55	203.8	22.5	399	7	W02419
C 56	203.8	22.5	429	2	BS501570
C 57	203.8	22.5	877	2	BQ949414
C 58	203.6	22.4	468	1	AL603499
C 59	203.6	22.4	866	5	BU102171
C 60	203.6	22.4	984	5	BO707135
C 61	203.6	22.4	4374	3	CR749501
C 62	203.2	22.4	643	9	AG129001
C 63	203.2	22.4	670	4	BM671184
C 64	203	22.4	321	2	AW511569
C 65	203	22.4	738	9	AG181502
C 66	202.8	22.4	462	5	BE140949
C 67	202.8	22.4	823	8	BQ438489
C 68	202.8	22.4	933	7	AQ741080
C 69	202.6	22.3	393	7	H58293
C 70	202.6	22.3	440	5	BM992670
C 71	202.6	22.3	534	5	BX283237
C 72	202.6	22.3	687	9	AG123074
C 73	202.6	22.3	719	4	BM679548
C 74	202.6	22.3	817	2	BE747923
C 75	202.6	22.3	973	5	BK36546
C 76	202.6	22.3	3443	3	HSW801859
C 77	202.6	22.3	7004	3	CR749209
C 78	202.4	22.3	556	7	CK822725
C 79	202.2	22.3	447	2	BP901147
C 80	202.2	22.3	498	7	CR542874
C 81	202.2	22.3	586	6	CA406158
C 82	202.2	22.3	636	5	BM971480
C 83	202.2	22.3	693	5	AG170941
C 84	202.2	22.3	701	9	AG170941
C 85	202.2	22.3	799	6	CD655686
C 86	202.2	22.3	924	5	BO710195
C 87	202	22.3	320	5	BU588558
C 88	202	22.3	588	8	AQ373949
C 89	202	22.3	661	9	AG059678
C 90	202	22.3	673	8	AQ375515
C 91	201.8	22.2	455	8	AQ37381
C 92	201.6	22.2	560	8	AQ479702
C 93	201.6	22.2	498	8	AQ479619
C 94	201.6	22.2	199	3	AG064568
C 95	201.6	22.2	168	3	CR623156
C 96	201.4	22.2	383	1	AI369076
C 97	201.4	22.2	394	7	CN278335

CA391442	cel5c09.y
AZ519506	RPCI-11-3
AV700758	APV00758
AV764406	AV764406
H59651	Yr35c02.t1
AQ784619	HS_3248-A
BK484839	DKFZP686K
AA829665	od97a11.8
BI254712	602976092
AG126921	Pan tregl
AG126921	Pan tregl
AG064993	Pan tregl
BK494015	DKFZP781J
BF957905	PM1-NN120
BM66389	UI-R-COI-
BP301691	BP301691
AA720582	mw21b01.8
AQ752732	HS_3568_B
BC021103	Homo gap1
BS1474	CIT9788K-A-
BP968874	602270846
CN264016	170004241
CN275741	170006000
BC819887	602781970
BC019875	Homo gap1
BO631269	1118h07.x
BU790005	in49d06.x
AQ310879	CIT-HSP-2
AQ316808	RPCI11-3P
AG088570	Pan tregl
BQ271642	IK16i01.x
W02419	zas1a04.t1
BS501570	ht62d07.x
BQ949414	AGENCOURT
AL603499	DKFZP686L
BU102171	PRODS1GID
BO707135	AGENCOURT
CR749501	Homo gap1
AG129001	Pan tregl
BM671184	UI-E-COI-
AW511569	xu60a07.x
AG181502	Pan tregl
BE140949	MRO-HT006
BQ438489	AGENCOURT
AG741080	HS_2272.A
H58293	Yr20F07.t1
BM992670	UI-H-DFO-
BX283237	EX283237
AG123074	Pan tregl
BM679548	UI-B-E00-
BE747923	601580282
BK36546	BK436546
AL16891	Homo gap1
CR749209	Homo gap1
CK822725	1697a04.y
BP901147	IL2-MT01.7
CR542874	DKFZP459W
CA406158	1002307.H
BM971480	UI-CF-BN1
AG170941	Pan tregl
CD655686	AGENCOURT
BO710195	AGENCOURT
BU588558	AGENCOURT
AQ373949	RPCI11-15
AG059678	Pan tregl
AQ375515	RPCI11-15
AQ37381	CIT-HSP-2
AQ479702	RPCI-11-2
AQ479619	RPCI-11-2
AG064568	Pan tregl
CR623156	full-1eng
AI369076	gw29h03.x
CN278335	170006002

C 98	201.4	22.2	652	8	AQ26609	RPCI11-75	171	199.2	22.0	577	8	AQ483173
C 99	201.4	22.2	683	9	AG177245	Pan t1rog1	172	199.2	22.0	579	7	CR545097
C 100	201.4	22.2	894	8	AQ738714	HS_5382_B	173	199.2	22.0	635	7	CN265093
C 101	201.2	22.2	368	1	AA623009	np79h05.8	174	199.2	22.0	657	9	AG150142
C 102	201.2	22.2	417	1	AV733634	AV733634	175	199.2	22.0	678	7	CN341129
C 103	201.2	22.2	420	8	AQ036829	CIT-HSP-2	176	199.2	22.0	684	7	CR766437
C 104	201.2	22.2	494	8	AQ228611	HS_2009_A	177	199.2	22.0	678	7	AQ263765
C 105	201.2	22.2	533	7	CN480174	UI-H-EDU-	178	199.2	22.0	370	8	AQ158606
C 106	201.2	22.2	618	6	CA335336	CA335336	179	199.2	22.0	559	1	AUI58606
C 107	201.2	22.2	680	5	BX114339	EX114339	180	199.2	22.0	612	5	BUI95255
C 108	201.2	22.2	1548	3	CR594735	EX114339	181	199.2	22.0	617	8	AQ197170
C 109	201.2	22.2	485	8	B69763	CR594735	182	199.2	22.0	649	5	BM991864
C 110	201.2	22.2	652	5	BX951325	B69763	183	199.2	22.0	724	8	B2612696
C 111	201.2	22.2	750	9	AG081408	AG081408	184	199.2	22.0	374	1	A1282479
C 112	201.2	22.2	938	8	AP101690	AP101690	185	199.2	22.0	432	5	AQ472783
C 113	200.8	22.1	353	7	CN271795	CN271795	186	199.2	22.0	349	7	B0637025
C 114	200.8	22.1	372	7	BM991270	UI-H-DIO-	187	199.2	22.0	769	6	CD370173
C 115	200.8	22.1	723	7	CR789995	CR789995	188	199.2	22.0	897	5	AQ744210
C 116	200.8	22.1	854	6	CD171905	CD171905	189	199.2	22.0	921	8	BX370271
C 117	200.8	22.1	1126	5	BX333363	BX333363	190	199.2	22.0	349	7	T24036
C 118	200.6	22.1	449	2	BE042511	BE042511	191	199.2	22.0	354	4	BM662676
C 119	200.6	22.1	485	8	AQ219222	HS_3245_B	192	199.2	22.0	515	2	AM177869
C 120	200.6	22.1	503	4	BM510027	BM510027	193	199.2	22.0	548	7	CN414083
C 121	200.6	22.1	744	8	BZ599872	BZ599872	194	199.2	22.0	679	2	BS392753
C 122	200.6	22.1	785	5	BUS67231	BUS67231	195	199.2	22.0	694	6	CA420398
C 123	200.6	22.1	799	5	BUS54310	BUS54310	196	199.2	22.0	324	4	BM671251
C 124	200.4	22.1	360	1	A1254267	A1254267	197	199.2	22.0	390	7	CN272500
C 125	200.4	22.1	507	1	AA601712	AA601712	198	199.2	22.0	426	7	CN395233
C 126	200.4	22.1	687	9	AG135036	AG135036	199	199.2	22.0	914	5	CN267428
C 127	200.4	22.1	808	4	BG622731	BG622731	200	199.2	22.0	964	7	BUI17014
C 128	200.4	22.1	1750	3	AF119908	AF119908	201	199.2	22.0	922	5	BUS01973
C 129	200.2	22.1	416	1	AV693536	AV693536	202	199.2	22.0	369	5	BX470473
C 130	200.2	22.1	420	2	BE062545	BE062545	203	199.2	22.0	404	8	B91764
C 131	200.2	22.1	421	1	AV691556	AV691556	204	199.2	22.0	453	8	AQ176505
C 132	200.2	22.1	569	7	CN274765	CN274765	205	199.2	22.0	493	2	AM328531
C 133	200.2	22.1	654	7	CR791150	CR791150	206	199.2	22.0	504	4	BI715158
C 134	200.2	22.1	690	4	BF971234	BF971234	207	199.2	22.0	510	1	AV756056
C 135	200.2	22.1	1034	4	BM806909	BM806909	208	199.2	22.0	562	7	CK818567
C 136	200.2	22.1	557	4	BM991139	BM991139	209	199.2	22.0	580	5	BP264216
C 137	200.2	22.1	586	5	BX951238	BX951238	210	199.2	22.0	648	8	AQ309277
C 138	200.2	22.1	621	9	AG102562	AG102562	211	199.2	22.0	669	5	BUI950624
C 139	200.2	22.1	665	9	AG045689	AG045689	212	199.2	22.0	670	9	AG164774
C 140	199.8	22.0	439	1	A1355559	q175f05.x	213	198.2	21.9	681	9	AG079336
C 141	199.8	22.0	466	8	AQ483846	AQ483846	214	198.2	21.9	716	9	AG002485
C 142	199.8	22.0	564	7	CN413054	CN413054	215	198.2	21.9	1238	7	BM455282
C 143	199.8	22.0	581	2	AM970987	AM970987	216	198.2	21.9	386	7	CF135158
C 144	199.8	22.0	595	8	AQ424714	CITBI-EL-	217	198.2	21.8	387	8	AQ196676
C 145	199.8	22.0	730	5	BUI61624	UI-H-DFO-	218	198.2	21.8	504	9	BUI98009
C 146	199.8	22.0	837	5	BX486445	BX486445	219	198.2	21.8	543	5	CI423119
C 147	199.8	22.0	840	1	AL706641	AL706641	220	198.2	21.8	636	2	BE140955
C 148	199.8	22.0	919	3	BC013247	BC013247	221	198.2	21.8	657	8	AQ477136
C 149	199.8	22.0	960	6	CD245816	CD245816	222	198.2	21.8	887	5	BQ423685
C 150	199.6	22.0	357	1	A1031759	A1031759	223	198.2	21.8	969	3	CR623410
C 151	199.6	22.0	423	8	AQ059624	CIT-HSP-2	224	197.8	21.8	420	5	BQ822326
C 152	199.6	22.0	458	2	AM151247	AM151247	225	197.8	21.8	442	2	AM514844
C 153	199.6	22.0	572	8	AQ763732	HS_3186_A	226	197.8	21.8	442	5	BX280439
C 154	199.6	22.0	680	5	BM985796	BM985796	227	197.8	21.8	467	8	AQ349390
C 155	199.6	22.0	681	5	BQ016777	UI-H-EDU-	228	197.8	21.8	475	2	AM008184
C 156	199.6	22.0	684	5	BQ772479	UI-H-FEO-	229	197.8	21.8	478	7	CN265094
C 157	199.6	22.0	736	5	BQ000441	UI-H-DFO-	230	197.8	21.8	549	9	CB177313
C 158	199.6	22.0	862	4	BG762519	BG762519	231	197.8	21.8	551	6	CA440586
C 159	199.6	22.0	876	6	CD556766	CD556766	232	197.8	21.8	583	5	BP301697
C 160	199.6	22.0	909	4	BG034698	BG034698	233	197.8	21.8	590	8	AO537619
C 161	199.6	22.0	941	5	BX451504	BX451504	234	197.8	21.8	664	7	CN265061
C 162	199.6	22.0	3128	3	CR627380	CR627380	235	197.8	21.8	672	5	BUI61955
C 163	199.6	22.0	3243	3	HSM805448	HSM805448	236	197.8	21.8	699	5	BQ712205
C 164	199.4	22.0	321	5	BUI958280	BUI958280	237	197.6	21.8	350	1	AV743179
C 165	199.4	22.0	379	8	AO580711	RPCI-11-4	238	197.6	21.8	453	5	BUT26699
C 166	199.4	22.0	558	5	BUS80548	in35c05.x	239	197.6	21.8	479	1	A1744963
C 167	199.4	22.0	604	5	BM990713	UI-H-DIO-	240	197.6	21.8	662	9	AG011122
C 168	199.4	22.0	631	9	AG050042	Pan t1rog1	241	197.6	21.8	707	5	BX488461
C 169	199.4	22.0	4974	3	HSM804886	AL833573	242	197.6	21.8	843	5	BQ421400
C 170	199.2	22.0	427	1	A1123488	ga01f01.x	243	197.6	21.8	957	5	BQ441618

AQ26609	RPCI11-75	171	199.2	22.0	577	8	AQ483173
AG177245	Pan t1rog1	172	199.2	22.0	579	7	CR545097
AQ738714	HS_5382_B	173	199.2	22.0	635	7	CN265093
AA623009	np79h05.8	174	199.2	22.0	657	9	AG150142
AV733634	AV733634	175	199.2	22.0	678	7	CN341129
AQ036829	CIT-HSP-2	176	199.2	22.0	684	7	CR766437
AQ228611	HS_2009_A	177	199.2	22.0	678	7	AQ263765
CN480174	UI-H-EDU-	178	199.2	22.0	370	8	AUI58606
CA335336	CA335336	179	199.2	22.0	559	1	AUI58606
BX114339	EX114339	180	199.2	22.0	612	5	BUI95255
CR594735	EX114339	181	199.2	22.0	617	8	AQ197170
B69763	CR594735	182	199.2	22.0	649	5	BM991864
BX951325	B69763	183	199.2	22.0	724	8	B2612696
DKF2P453P	DKF2P453P	184	199.2	22.0	374	1	A1282479
AG081408	Pan t1rog1	185	199.2	22.0	432	5	AQ472783
AP101690	AP101690	186	199.2	22.0	349	7	B0637025
CN271795	CN271795	187	199.2	22.0	769	6	CD370173
UI-H-DIO-	UI-H-DIO-	188	199.2	22.0	897	5	AQ744210
DKF2P453P	DKF2P453P	189	199.2	22.0	921	8	BX370271
BX333363	BX333363	190	199.2	22.0	349	7	T24036
BE042511	BE042511	191	199.2	22.0	354	4	BM662676
HS_3245_B	HS_3245_B	192	199.2	22.0	515	2	AM177869
1977a04.x	1977a04.x	193	199.2	22.0	548	7	CN414083
BZ599872	BZ599872	194	199.2	22.0	679	2	BS392753
WHACH93TR	WHACH93TR	195	199.2	22.0	694	6	CA420398
AGENCOURT	AGENCOURT	196	199.2	22.0	324	4	BM671251
UI-H-DIO-	UI-H-DIO-	197	199.2	22.0	390	7	CN272500
qy33f07.x	qy33f07.x	198	199.2	22.0	426	7	CN395233
mo03805.8	mo03805.8	199	199.2	22.0	914	5	CN267428
Pan t1rog1	Pan t1rog1	200	199.2	22.0	964	7	BUI17014
602647510	602647510	201	199.2	22.0	922	5	BUS01973
AV693536	AV693536	202	199.2	22.0	369	5	BX470473
CV4-BT025	CV4-BT025	203	199.2	22.0	404	8	B91764
AV691556	AV691556	204	199.2	22.0	453	8	AQ176505
170006000	170006000	205	199.2	22.0	493	2	AM328531
DKF2P469E	DKF2P469E	206	199.2	22.0	504	4	BI715158
602273252	602273252	207	199.2	22.0	510	1	AV756056
AGENCOURT	AGENCOURT	208	199.2	22.0	562	7	CK818567
UI-H-DIO-	UI-H-DIO-	209	199.2	22.0	580	5	BP264216
DKF2P781P	DKF2P781P	210	199.2	22.0	648	8	AQ309277
Pan t1rog1	Pan t1rog1	211	199.2	22.0			

C 244	197.6	21.8	993	3	AFJ18326	Homo sapi	317	196.6	21.7	582	5	BP267287
C 245	197.6	21.8	3204	3	AL832994	Homo sapi	318	196.6	21.7	582	5	BP275852
C 246	197.6	21.8	5093	3	BX649002	Homo sapi	319	196.6	21.7	582	5	BP292016
C 247	197.4	21.8	324	1	AI247118		320	196.6	21.7	583	5	BP268005
C 248	197.4	21.8	330	5	BUE55123		321	196.6	21.7	596	5	BX484036
C 249	197.4	21.8	344	1	AIS90404	tE10D03.x	322	196.6	21.7	601	1	AL708507
C 250	197.4	21.8	401	8	AQ669103	HS_5414.A	323	196.6	21.7	635	8	AO313550
C 251	197.4	21.8	492	5	BQ706631	AGENCOURT	324	196.6	21.7	637	4	BM691791
C 252	197.4	21.8	541	5	BM993720	UI-H-DHO-	325	196.6	21.7	645	7	CN362346
C 253	197.4	21.8	554	5	BX494380	DXFZP79C	326	196.6	21.7	652	9	AG116098
C 254	197.4	21.8	613	5	BM990533	BM990533 UI-H-DHO-	327	196.6	21.7	661	2	BE177530
C 255	197.4	21.8	677	7	CK004046	AGENCOURT	328	196.6	21.7	701	7	CF125387
C 256	197.4	21.8	723	7	AG143729	Pan tEogl	329	196.6	21.7	777	4	BI093486
C 257	197.4	21.8	733	6	CA308850	UI-H-FT1-	330	196.6	21.7	824	8	BZ611785
C 258	197.4	21.8	902	6	BF034649	601455087	331	196.6	21.7	879	5	BX414544
C 259	197.4	21.8	966	5	BQ227117	AGENCOURT	332	196.6	21.7	1000	5	BQ049398
C 260	197.4	21.8	949	5	BQ950110	AGENCOURT	333	196.6	21.7	1023	4	BM452492
C 261	197.2	21.7	319	1	AV683406	AV683406	334	196.6	21.7	1143	5	BM918656
C 262	197.2	21.7	412	8	BM040851	603614535	335	196.6	21.7	1359	8	AP101912
C 263	197.2	21.7	436	8	AZ518582	RPCI-11-1	336	196.6	21.7	1588	3	CN596829
C 264	197.2	21.7	470	1	AI760835	WH96F11.x	337	196.6	21.7	3536	3	CR749620
C 265	197.2	21.7	427	1	AI924950	WM26D03.x	338	196.6	21.7	3974	3	HSM805841
C 266	197.2	21.7	516	8	AQ651270	HS_5358.A	339	196.6	21.7	4747	3	AA224966
C 267	197.2	21.7	642	8	CN276868	17006001	340	196.4	21.7	458	2	AM772513
C 268	197.2	21.7	654	8	AQ478207	RPCI-11-2	341	196.4	21.7	464	8	AQ632383
C 269	197.2	21.7	751	1	AI188382	qG13F06.x	342	196.4	21.7	619	8	BH609896
C 270	197.2	21.7	384	1	AI521360	t105d10.x	343	196.4	21.7	1042	5	BX377759
C 271	197	21.7	399	4	BG223374	naJ76a09.	344	196.4	21.7	3744	5	BC018955
C 272	197	21.7	417	1	AV697609	AV697609	345	196.4	21.7	319	5	AA503307
C 273	197	21.7	574	7	CR559874	DXFZP459L	346	196.2	21.6	352	1	AA503307
C 274	197	21.7	633	9	AG144698	Pan tEogl	347	196.2	21.6	372	2	BH328288
C 275	197	21.7	635	9	CR768142	DXFZP469G	348	196.2	21.6	456	1	AI801563
C 276	197	21.7	741	8	AZ517850	RPCI-11-1	350	196.2	21.6	481	8	B66178
C 277	197	21.7	770	5	BX090291	BX090291	351	196.2	21.6	493	8	B36003
C 278	197	21.7	775	4	BI860178	603387374	352	196.2	21.6	498	1	AUI44397
C 279	197	21.7	826	5	BQ438665	AGENCOURT	353	196.2	21.6	567	5	BP267172
C 280	197	21.7	866	5	BQ172464	AGENCOURT	354	196.2	21.6	568	7	AM813106
C 281	197	21.7	884	5	BQ711287	BQ711287	355	196.2	21.6	636	7	CN480509
C 282	197	21.7	893	5	BO706660	AGENCOURT	356	196.2	21.6	722	2	BF383027
C 283	197	21.7	900	2	BE888692	BE888692	357	196.2	21.6	1383	3	CR623768
C 284	197	21.7	903	2	BE867712	601443272	358	196.2	21.6	401	2	AM341882
C 285	197	21.7	3775	3	CR627381	Homo sapi	359	196.2	21.6	451	8	AQ394853
C 286	196.8	21.7	323	1	AA774223	AB55E12.B	360	196	21.6	521	2	AM957502
C 287	196.8	21.7	342	1	AI174703	HA2407.8	361	196	21.6	590	6	CD707806
C 288	196.8	21.7	390	1	AA719543		362	196	21.6	663	9	AG051773
C 289	196.8	21.7	416	2	BE062476	AV4-BT025	363	196	21.6	694	9	AG015017
C 290	196.8	21.7	433	8	AQ342192	RPCI11-12	364	196	21.6	770	9	AG002921
C 291	196.8	21.7	439	4	BM127488	1e95h07.Y	365	196	21.6	778	6	CB963857
C 292	196.8	21.7	477	1	AL709726	DXFZP686H	366	196	21.6	851	1	AUI20423
C 293	196.8	21.7	478	1	AI761677	WH99D07.x	367	196	21.6	1058	4	BM554734
C 294	196.8	21.7	483	8	AQ828636	HS_4832.A	368	195.8	21.6	356	1	AA349710
C 295	196.8	21.7	504	5	BX490571	DXFZP68EE	369	195.8	21.6	5604	3	HSMA807067
C 296	196.8	21.7	532	4	BM743761	K-BST0017	370	195.8	21.6	362	1	AA550528
C 297	196.8	21.7	572	4	BM743761	K-BST0017	371	195.8	21.6	428	8	BP431064
C 298	196.8	21.7	587	4	BZ610289	AV728974	372	195.8	21.6	443	5	AQ589677
C 299	196.8	21.7	604	1	AV729714	AV729714	373	195.8	21.6	512	8	AQ120174
C 300	196.8	21.7	685	7	CK001797	AGENCOURT	374	195.8	21.6	540	1	AL659257
C 301	196.8	21.7	709	5	BUE74938	UI-CF-DUO	375	195.8	21.6	628	1	AI065031
C 302	196.8	21.7	718	8	BZ773121	mcv62d01.	376	195.8	21.6	658	5	BX486751
C 303	196.8	21.7	7230	3	CR615928	full-1eng	377	195.8	21.6	669	5	BM997858
C 304	196.8	21.7	5110	3	HSMB804874		378	195.8	21.6	732	8	AQ890095
C 305	196.8	21.7	5641	3	BX538234	Homo sapi	379	195.8	21.6	863	8	AQ738509
C 306	196.6	21.7	313	4	HSMB710087	UI-E-COI-	380	195.8	21.6	884	6	AO738492
C 307	196.6	21.7	352	1	AI572680	tr78a09.x	381	195.8	21.6	892	6	CD518383
C 308	196.6	21.7	380	2	BE246411	TCBAP1D46	382	195.6	21.6	354	6	CD485194
C 309	196.6	21.7	400	2	BF920612	QVO-NT015	383	195.6	21.6	365	5	AQ085904
C 310	196.6	21.7	426	1	AI914748	ct01e09.x	384	195.6	21.6	375	1	AI223968
C 311	196.6	21.7	436	2	BF816190	MR2-C1012	385	195.6	21.6	377	1	AA657392
C 312	196.6	21.7	461	2	AM151848	xf71f12.x	386	195.6	21.6	384	7	AI281561
C 313	196.6	21.7	490	5	BQ639303	hD3j308.y	387	195.6	21.6	392	1	AA484892
C 314	196.6	21.7	493	1	AI733523	yJ89h06.y	388	195.6	21.6	396	1	AI355103
C 315	196.6	21.7	578	5	BP267532	BP267532	389	195.6	21.6	397	8	AQ214855
C 316	196.6	21.7	579	5	BP266615	BP266615						
C 244	197.6	21.8	993	3	AFJ18326	Homo sapi	317	196.6	21.7	582	5	BP267287
C 245	197.6	21.8	3204	3	AL832994	Homo sapi	318	196.6	21.7	582	5	BP275852
C 246	197.6	21.8	5093	3	BX649002	Homo sapi	319	196.6	21.7	582	5	BP292016
C 247	197.4	21.8	324	1	AI247118		320	196.6	21.7	583	5	BP268005
C 248	197.4	21.8	330	5	BUE55123		321	196.6	21.7	596	5	BX484036
C 249	197.4	21.8	344	1	AIS90404	tE10D03.x	322	196.6	21.7	601	1	AL708507
C 250	197.4	21.8	401	8	AQ669103	HS_5414.A	323	196.6	21.7	635	8	AO313550
C 251	197.4	21.8	492	5	BQ706631	AGENCOURT	324	196.6	21.7	637	4	BM691791
C 252	197.4	21.8	541	5	BM993720	UI-H-DHO-	325	196.6	21.7	645	7	CN362346
C 253	197.4	21.8	554	5	BX494380	DXFZP79C	326	196.6	21.7	652	9	AG116098
C 254	197.4	21.8	613	5	BM990533	BM990533 UI-H-DHO-	327	196.6	21.7	661	2	BE177530
C 255	197.4	21.8	677	7	CK004046	AGENCOURT	328	196.6	21.7	701	7	CF125387
C 256	197.4	21.8	723	7	AG143729	Pan tEogl	329	196.6	21.7	777	4	BI093486
C 257	197.4	21.8	733	6	CA308850	UI-H-FT1-	330	196.6	21.7	824	8	BZ611785
C 258	197.4	21.8	902	6	BF034649	601455087	331	196.6	21.7	879	5	BX414544
C 259	197.4	21.8	966	5	BQ227117	AGENCOURT	332	196.6	21.7	1000	5	BQ049398
C 260	197.4	21.8	949	5	BQ950110	AGENCOURT	333	196.6	21.7	1023	4	BM452492
C 261	197.2	21.7	319	1	AV683406	AV683406	334	196.6	21.7	1143	5	BM918656
C 262	197.2	21.7	412	8	BM040851	603614535	335	196.6	21.7	1359	8	AP101912
C 263	197.2	21.7	436	8	AZ518582	RPCI-11-1	336	196.6	21.7	1588	3	CN596829
C 264	197.2	21.7	470	1	AI760835	WH96F11.x	337	196.6	21.7	3536	3	CR749620
C 265	197.2	21.7	427	1	AI924950	WM26D03.x	338	196.6	21.7	3974	3	HSM805841
C 266	197.2	21.7	516	8	AQ651270	HS_5358.A	339	196.6	21.7	4747	3	AA224966
C 267	197.2	21.7	642	8	CN276868	17006001	340	196.4	21.7	458	2	AM772513
C 268	197.2	21.7	654	8	AQ478207	RPCI-11-2	341	196.4	21.7	464	8	AQ632383
C 269	197.2	21.7	751	1	AI188382	qG13F06.x	342	196.4	21.7	619	8	BH609896
C 270	197.2	21.7	384	1	AI521360	t105d10.x	343	196.4	21.7	1042	5	BX377759
C 271	197	21.7	399	4	BG223374	naJ76a09.	344	196.4	21.7	3744	5	BC018955
C 272	197	21.7	417	1	AV697609	AV697609	345	196.4	21.7	319	5	AA503307
C 273	19											

C 390	195.6	21.6	441	8	A2521019		C 463	195	21.5	680	9	AG077619	AG077619	Pan	trogl	
C 391	195.6	21.6	480	7	CN269107		C 464	195	21.5	682	9	AG181743	AG181743	Pan	trogl	
C 392	195.6	21.6	500	8	AQ248325		C 465	195	21.5	705	7	CN278633	CN278633	170006003		
C 393	195.6	21.6	521	5	BU617227		C 466	195	21.5	759	5	BU854207	BU854207	AGNENCOURT		
C 394	195.6	21.6	529	8	B92837	CIT-HSP-216	C 467	195	21.5	722	1	AU136365	AU136365			
C 395	195.6	21.6	566	8	BU072318	Im45C07.x	C 468	195	21.5	885	8	AQ739135	AQ739135	HS_5387_B		
C 396	195.6	21.6	573	2	AW974923	ES1387028	C 469	195	21.5	886	8	AQ739494	HS_5387_B			
C 397	195.6	21.6	580	1	AU150583	AU150583	C 470	195	21.5	910	5	BU850247	AGNENCOURT			
C 398	195.6	21.6	580	5	BP336490	BP336490	C 471	195	21.5	915	5	BU149187	AGNENCOURT			
C 399	195.6	21.6	580	5	BU053726	AGNENCOURT	C 472	195	21.5	924	4	BG697612	602660853			
C 400	195.6	21.6	598	5	BU017808	UT-H-ED0-	C 473	195	21.5	998	5	EX381716	EX381716			
C 401	195.6	21.6	609	9	AG149236	Pan	trogl	C 474	195	1007	5	BZ611150	WHAC165TF			
C 402	195.6	21.6	616	9	BU617236	UT-H-DP0-	C 475	195	21.5	1035	5	BQ217751	AF130079			
C 403	195.6	21.6	619	8	B58514	CIT-HSP-201	C 476	195	21.5	1769	3	AF130079	BU149187			
C 404	195.6	21.6	660	7	CR545328	DXF2P459J	C 477	195	21.5	1850	3	BC025771	BC025771	Homo	sap1	
C 405	195.6	21.6	684	8	AO633073	RPC1-11-4	C 478	194.8	21.5	340	1	AA666295	ac39a10.8			
C 406	195.6	21.6	702	9	AG153097	Pan	trogl	C 479	194.8	383	1	AV655282	AV655282			
C 407	195.6	21.6	729	7	CN302098	170006001	C 480	194.8	21.5	394	1	AI732690	AI732690	nc75d11.x		
C 408	195.6	21.6	731	1	AI687343	tp86f08.x	C 481	194.8	21.5	420	1	AA467912	AA467912	nc75d11.x		
C 409	195.6	21.6	791	5	BU943219	AGNENCOURT	C 482	194.8	21.5	434	1	AA487569	ab23f03.8			
C 410	195.6	21.6	836	4	BG771122	602719716	C 483	194.8	21.5	438	1	AI702018	AI702018	tc20c12.x		
C 411	195.6	21.6	977	3	CR600792	full-1em9	C 484	194.8	21.5	457	8	AQ391790	AQ391790	CITBT-EL-		
C 412	195.6	21.6	1111	5	EX437747	EX437747	C 485	194.8	21.5	532	1	AL036896	AL036896	DXF2P664A		
C 413	195.4	21.5	342	5	EX480789	DXF2P686D	C 486	194.8	21.5	537	8	AQ406948	AQ406948	HS_5113_A		
C 414	195.4	21.5	352	1	AI701898	tcq19e03.x	C 487	194.8	21.5	553	9	AG040162	AG040162	Pan	trogl	
C 415	195.4	21.5	421	1	AI473671	tm02h06.x	C 488	194.8	21.5	653	9	AG054232	AG054232	Pan	trogl	
C 416	195.4	21.5	427	2	AW880986	OVO-OT003	C 489	194.8	21.5	658	9	AG115757	AG115757	Pan	trogl	
C 417	195.4	21.5	439	8	AQ768011	HS_3189_A	C 490	194.8	21.5	733	8	AQ546618	AQ546618	CITBT-EL-		
C 418	195.4	21.5	450	7	TS1920	Y028B02.B1	C 491	194.8	21.5	825	8	BZ601462	BZ601462	WHAAT45TR		
C 419	195.4	21.5	505	7	EX952682	DXF2P781L	C 492	194.8	21.5	835	8	EX438918	EX438918	HS_5387_B		
C 420	195.4	21.5	510	8	AQ477081	CITBT-EL-	C 493	194.8	21.5	933	8	AQ743038	AQ743038	HS_5387_B		
C 421	195.4	21.5	510	5	BU590031	AGNENCOURT	C 494	194.8	21.5	1107	5	BM438918	BM438918	HS_5387_B		
C 422	195.4	21.5	528	7	CN263775	170004241	C 495	194.8	21.5	6789	1	HSMB07629	HSMB07629			
C 423	195.4	21.5	578	7	CR818107	ic139c04.y	C 496	194.6	21.5	398	1	AI798521	AI798521	tr36e12.x		
C 424	195.4	21.5	586	1	AI207422	HA2764_Hu	C 497	194.6	21.5	440	8	AQ027499	AQ027499	CIT-HSP-2		
C 425	195.4	21.5	615	8	AQ455915	AG122688	C 498	194.6	21.5	449	8	AQ062661	AQ062661	CIT-HSP-2		
C 426	195.4	21.5	714	9	AG122688	Pan	trogl	C 499	194.6	21.5	457	8	B55517	B55517	CIT-HSP-387	
C 427	195.2	21.5	359	6	F23338	HSFDP20157_H	C 500	194.6	21.5	508	8	AQ152893	AQ152893	HS_3033_A		
C 428	195.2	21.5	360	6	CI4614	CI4614	C 501	194.6	21.5	535	5	AX953337	AX953337	CITBT-EL-		
C 429	195.2	21.5	385	6	CR296760	12822054_-	C 502	194.6	21.5	539	8	AQ544113	AQ544113			
C 430	195.2	21.5	405	1	AI280535	qu04h02.x	C 503	194.6	21.5	619	7	CF146583	CF146583	UT-HF-CB0		
C 431	195.2	21.5	415	5	EX116453	EX116453	C 504	194.6	21.5	658	9	AG087949	AG087949	Pan	trogl	
C 432	195.2	21.5	437	5	EX489723	DXF2P686B	C 505	194.6	21.5	664	1	AL120004	AL120004	DXF2P761G		
C 433	195.2	21.5	443	8	AQ434649	HS_5086_B	C 506	194.6	21.5	669	5	EX951401	EX951401	DXF2P781H		
C 434	195.2	21.5	488	4	BM505317	ic93c04.x	C 507	194.6	21.5	675	5	BM991716	BM991716	UT-H-DP1-		
C 435	195.2	21.5	503	1	AA604149	nc69B05.8	C 508	194.6	21.5	701	9	AG144939	AG144939	Pan	trogl	
C 436	195.2	21.5	542	5	BU001553	UT-H-DP1-	C 509	194.6	21.5	704	7	CF122920	CF122920	UT-HF-CB0		
C 437	195.2	21.5	543	1	AA019919	z663g05.8	C 510	194.6	21.5	706	9	AV759354	AV759354			
C 438	195.2	21.5	552	2	AW970588	EST382669	C 511	194.6	21.5	708	9	AG154962	AG154962	Pan	trogl	
C 439	195.2	21.5	602	5	BU657458	cl24e02.z	C 512	194.6	21.5	712	9	AG095201	AG095201	Pan	trogl	
C 440	195.2	21.5	633	9	AG094873	Pan	trogl	C 513	194.6	21.5	877	5	BX457314	BX457314	EX402079	
C 441	195.2	21.5	656	4	BG898542	HOA56-1-C	C 514	194.6	21.5	1071	5	EX402079	EX402079			
C 442	195.2	21.5	660	5	AG011123	Homo	sap1	C 515	194.6	1210	3	CR598366	CR598366	full-1em9		
C 443	195.2	21.5	681	5	BQ477500	ik87g11.x	C 516	194.6	21.5	1210	3	CR598366	CR598366			
C 444	195.2	21.5	769	8	AQ090076	HS_3034_B	C 517	194.4	21.4	332	1	AI311796	AI311796	gc71e11.x		
C 445	195.2	21.5	769	8	AG090076	HS_3034_B	C 518	194.4	21.4	392	1	AI311796	AI311796	gc71e11.x		
C 446	195.2	21.5	951	5	BO710495	AGNENCOURT	C 519	194.4	21.4	402	2	BG219888	BG219888	REST41806		
C 447	195.2	21.5	1758	3	BC004550	Homo	sap1	C 520	194.4	412	2	BE062478	BE062478	QV4-ET025		
C 448	195	21.5	353	2	BF805088	ILS-C1015	C 521	194.4	21.4	427	2	AW272815	AW272815	xt42d06.x		
C 449	195	21.5	393	8	AQ771301	HS_2120_B	C 522	194.4	21.4	432	8	B31519	B31519	HS_1011-A1-		
C 450	195	21.5	400	1	AI268818	gc040h06.x	C 523	194.4	21.4	477	8	AQ162639	AQ162639	HS_3035_A		
C 451	195	21.5	447	1	AI281622	qu58g05.x	C 524	194.4	21.4	512	2	BF846619	BF846619	QV0-EN005		
C 452	195	21.5	459	5	AX481314	DXF2P686T	C 525	194.4	21.4	523	4	BM504793	BM504793	ic99e09.x		
C 453	195	21.5	468	7	CN348180	170005319	C 526	194.4	21.4	526	5	EX475994	EX475994	DXF2P686H		
C 454	195	21.5	488	7	CR824505	1g27c10.y	C 527	194.4	21.4	604	7	CR822516	CR822516			
C 455	195	21.5	527	7	CR554971	DXF2P469P	C 528	194.4	21.4	635	7	CR629762	CR629762	DXF2P469P		
C 456	195	21.5	527	8	AQ466047	HS_5073_B	C 529	194.4	21.4	647	2	AW979158	AW979158	EST131268		
C 457	195	21.5	530	7	CR544735	DXF2P459L	C 530	194.4	21.4	672	9	AG066531	AG066531	Pan	trogl	
C 458	195	21.5	559	7	CN348183	170004553	C 531	194.4	21.4	681	9	AG182173	AG182173	Pan	trogl	
C 459	195	21.5	566	5	BP266899	BP266899	C 532	194.4	21.4	686	9	AG117862	AG117862	Pan	trogl	
C 460	195	21.5	624	5	EX509953	DXF2P686B	C 533	194.4	21.4	688	9	AG182171	AG182171	Pan	trogl	
C 461	195	21.5	640	7	CF128614	UI-HF-ET0	C 534	194.4	21.4	699	4	BG570479	BG570479			
C 462	195	21.5	665	7	CN270895	170005999	C 535	194.4	21.4	816	5	BU173801	BU173801	AGNENCOURT		

C 536	194.4	21.4	826	5	BQ220083	BQ220083	AGENCOURT	C 609	194	21.4	1613	3	CR591695
537	194.4	21.4	907	5	BQ710503	BQ710503	AGENCOURT	C 610	193.8	21.4	263	4	BI007641
538	194.4	21.4	916	5	BF983617	BF983617	602304735	C 611	193.8	21.4	409	1	AA676592
C 539	194.4	21.4	986	5	BUS01670	BUS01670	AGENCOURT	C 612	193.8	21.4	426	2	AW771062
C 540	194.2	21.4	320	5	BUS87770	BUS87770	AGENCOURT	C 613	193.8	21.4	441	2	BF738059
C 541	194.2	21.4	354	8	AQ277656	AQ277656	CITBI-RI-	C 614	193.8	21.4	469	6	CD691341
C 542	194.2	21.4	368	7	N23099	N23099	YV43906.81	C 615	193.8	21.4	486	6	CA484153
C 543	194.2	21.4	421	8	AQ064654	AQ064654	HS_2210_A	C 616	193.8	21.4	521	8	AQ777326
544	194.2	21.4	433	6	CD237813	CD237813	FNPAPH01	C 617	193.8	21.4	551	2	AW576914
C 545	194.2	21.4	485	8	AA055647	AA055647	2175d03.8	C 618	193.8	21.4	616	6	CB067437
C 546	194.2	21.4	522	8	AQ139069	AQ139069	HS_3082_B	C 619	193.8	21.4	629	9	AG092046
C 547	194.2	21.4	522	8	AQ155894	AQ155894	HS_3197_B	C 620	193.8	21.4	630	7	CK430112
C 548	194.2	21.4	529	5	BQ637931	BQ637931	hdi16d01.y	C 621	193.8	21.4	630	7	CA310364
C 549	194.2	21.4	533	5	AU151751	AU151751	AU151751	C 622	193.8	21.4	632	6	CA031347
C 550	194.2	21.4	560	1	AU147849	AU147849	AU147849	C 623	193.8	21.4	646	8	AQ313437
C 551	194.2	21.4	573	1	BE143664	BE143664	MRO-HT016	C 624	193.8	21.4	665	5	AG041398
C 552	194.2	21.4	579	2	BE143664	BE143664	MRO-HT016	C 625	193.8	21.4	666	5	BX504233
C 553	194.2	21.4	608	1	AL706835	AL706835	UI-H-DI0-	C 626	193.8	21.4	704	9	AG117725
C 554	194.2	21.4	626	5	BQ016577	BQ016577	UI-H-DI0-	C 627	193.8	21.4	704	9	AG117725
C 555	194.2	21.4	634	5	BX480648	BX480648	DKF2p686J	C 628	193.8	21.4	733	5	BX645097
C 556	194.2	21.4	690	9	AG185250	AG185250	Pan t1091	C 629	193.8	21.4	829	8	AF102038
C 557	194.2	21.4	694	7	CF124970	CF124970	UI-H-ET0	C 630	193.8	21.4	1053	4	BF970033
C 558	194.2	21.4	698	6	BO183396	BO183396	UI-H-ET0	C 631	193.8	21.4	1064	5	BM906989
C 559	194.2	21.4	707	6	CA439571	CA439571	UI-H-ET0	C 632	193.8	21.4	1077	1	AL524675
C 560	194.2	21.4	716	7	AF101676	AF101676	AF101676	C 633	193.8	21.4	1102	7	AL569764
C 561	194.2	21.4	721	8	AF101676	AF101676	WHAET33TF	C 634	193.8	21.4	325	7	F00688
C 562	194.2	21.4	749	8	BZ606363	BZ606363	AGENCOURT	C 635	193.6	21.3	359	5	BX105637
C 563	194.2	21.4	857	5	BUI89543	BUI89543	AGENCOURT	C 636	193.6	21.3	359	5	AX124663
C 564	194.2	21.4	868	6	BP967724	BP967724	602287586	C 637	193.6	21.3	400	8	AQ124663
C 565	194.2	21.4	919	4	BO708108	BO708108	AGENCOURT	C 638	193.6	21.3	409	1	AI287380
C 566	194.2	21.4	934	5	BSM804841	BSM804841	ALB33528	C 639	193.6	21.3	427	8	AQ473288
C 567	194.2	21.4	3250	2	BF830256	BF830256	MR3-HN006	C 640	193.6	21.3	439	7	F45056
568	194	21.4	325	9	AG366257	AG366257	Homo bap1	C 641	193.6	21.3	506	4	BI439760
C 569	194	21.4	326	9	AG189419	AG189419	Homo bap1	C 642	193.6	21.3	506	8	AQ283914
C 570	194	21.4	326	9	BR445745	BR445745	Pan t1091	C 643	193.6	21.3	520	7	CN273753
C 571	194	21.4	343	2	BR445745	BR445745	nae40c02.	C 644	193.6	21.3	535	1	AL158095
C 572	194	21.4	403	8	AQ125355	AQ125355	HS_2168_A	C 645	193.6	21.3	543	5	BUI677401
C 573	194	21.4	413	1	AV761486	AV761486	AV761486	C 646	193.6	21.3	585	4	BM045436
C 574	194	21.4	427	8	AQ564751	AQ564751	HS_5361_A	C 647	193.6	21.3	639	9	AG019704
C 575	194	21.4	469	1	AA526542	AA526542	n160h10.8	C 648	193.6	21.3	661	9	AG033142
C 576	194	21.4	474	8	AQ474083	AQ474083	CITBI-RI-	C 649	193.6	21.3	677	8	AQ194211
C 577	194	21.4	482	8	AQ475209	AQ475209	CITBI-RI-	C 650	193.6	21.3	678	7	CR629996
C 578	194	21.4	490	2	BE142845	BE142845	MRO-HT015	C 651	193.6	21.3	680	8	AO484111
C 579	194	21.4	504	8	AQ727006	AQ727006	HS_5431_A	C 652	193.6	21.3	691	1	AV699555
C 580	194	21.4	508	2	AW819483	AW819483	RC5-ST029	C 653	193.6	21.3	692	8	AQ780023
C 581	194	21.4	515	1	AI860648	AI860648	w104c07.x	C 654	193.6	21.3	762	6	CB311081
C 582	194	21.4	544	1	AU148232	AU148232	UI-H-ET0-	C 655	193.6	21.3	763	8	AQ311398
C 583	194	21.4	566	2	AW966643	AW966643	EST378717	C 656	193.6	21.3	856	4	AQ750055
C 584	194	21.4	574	7	BP220813	BP220813	BP220813	C 657	193.6	21.3	903	4	BG120824
C 585	194	21.4	580	5	CD686671	CD686671	EST3192.h	C 658	193.6	21.3	920	5	BU957399
586	194	21.4	582	5	BP355272	BP355272	BP355272	C 659	193.6	21.3	1112	5	BU902296
C 587	194	21.4	585	5	BP217403	BP217403	BP217403	C 660	193.4	21.3	413	1	AI7616120
C 588	194	21.4	583	5	BP217403	BP217403	BP217403	C 661	193.4	21.3	419	2	AW243817
C 589	194	21.4	585	1	AU146999	AU146999	FLC5087.H	C 662	193.4	21.3	450	8	AO615941
C 590	194	21.4	588	1	AI144575	AI144575	FLC5087.H	C 663	193.4	21.3	450	8	AO615941
C 591	194	21.4	613	2	AW844636	AW844636	RC3-CN005	C 664	193.4	21.3	453	1	AI732682
C 592	194	21.4	651	5	BX478977	BX478977	DKF2p686F	C 665	193.4	21.3	522	5	BX494125
C 593	194	21.4	651	5	BM679573	BM679573	UI-E-EO-	C 666	193.4	21.3	523	8	AQ387570
C 594	194	21.4	675	4	BM679573	BM679573	UI-E-EO-	C 667	193.4	21.3	562	5	BQ086265
C 595	194	21.4	698	9	AG108221	AG108221	Pan t1091	C 668	193.4	21.3	570	7	CR542889
C 596	194	21.4	701	9	AG163691	AG163691	Pan t1091	C 669	193.4	21.3	571	7	CR822946
597	194	21.4	707	9	AG175061	AG175061	Pan t1091	C 670	193.4	21.3	589	8	AQ535498
598	194	21.4	726	6	CD639534	CD639534	AGENCOURT	C 671	193.4	21.3	620	9	CR154550
C 599	194	21.4	731	6	BU627512	BU627512	UI-H-FCO-	C 672	193.4	21.3	635	6	CB154550
C 600	194	21.4	742	6	CD239228	CD239228	FNPMA10	C 673	193.4	21.3	636	7	CR72671
601	194	21.4	750	2	BE890203	BE890203	601513183	C 674	193.4	21.3	640	9	AG014547
C 602	194	21.4	760	5	BX643228	BX643228	DKF2p781F	C 675	193.4	21.3	649	5	AG014547
C 603	194	21.4	775	5	BM905333	BM905333	AGENCOURT	C 676	193.4	21.3	669	5	BM060838
C 604	194	21.4	788	5	BQ009047	BQ009047	UI-H-EIO-	C 677	193.4	21.3	678	9	AG090115
C 605	194	21.4	800	1	AU140619	AU140619	UI-H-EIO-	C 678	193.4	21.3	685	8	BZ610285
C 606	194	21.4	824	8	BZ601516	BZ601516	WHAEP38TR	C 679	193.4	21.3	688	2	BF792103
607	194	21.4	899	4	BM453994	BM453994	AGENCOURT	C 680	193.4	21.3	2144	3	AF130089
C 608	194	21.4	1580	3	CR599858	CR599858	full1-Jeng	C 681	193.4	21.3	2144	3	AF130089

682	193.4	21.3	2856	3	HSMB803730	ALB32422	Homo sapi	c 755	192.8	21.3	523	8	A2517953	A2517953	RPCT-11-3
c 683	193.4	21.3	3201	5	CR749792	CR749792	Homo sapi	c 756	192.8	21.3	532	5	BU947715	BU947715	i056e02.x
c 684	193.2	21.3	3505	5	BUS36659	BUS36659	AGENCOURT	c 757	192.8	21.3	570	1	AUI45239	AUI45239	
c 685	193.2	21.3	347	1	AA809546	AA809546	nj43c09.b	c 758	192.8	21.3	584	8	AQ473656	AQ473656	CITBI-EI-
c 686	193.2	21.3	377	5	BU960486	BU960486	AGENCOURT	c 759	192.8	21.3	599	1	A1636422	A1636422	cz79c01.x
c 687	193.2	21.3	418	1	AA148618	AA148618	zoo9c07.b	c 760	192.8	21.3	605	8	AQ347764	AQ347764	RPCT11-13
c 688	193.2	21.3	452	1	A1446623	A1446623	lj25d05.x	c 761	192.8	21.3	609	1	AV702857	AV702857	
c 689	193.2	21.3	482	2	BRF30052	BRF30052	MR3-HNO05	c 762	192.8	21.3	612	7	CK905828	CK905828	i185e03.x
c 690	193.2	21.3	488	1	AA566127	AA566127	nfl3dl2.b	c 763	192.8	21.3	617	8	BL6477	BL6477	TPB.C
c 691	193.2	21.3	498	8	AQ285474	AQ285474	RPCT11-78	c 764	192.8	21.3	636	5	BA483679	BA483679	
c 692	193.2	21.3	512	5	BK642749	BK642749	DKE2p781G	c 765	192.8	21.3	651	9	AG037309	AG037309	Par tregl
c 693	193.2	21.3	550	6	CD687373	CD687373	EST3894.h	c 766	192.8	21.3	658	8	CK430849	CK430849	
c 694	193.2	21.3	560	1	AL602775	AL602775	DKE2p6661	c 767	192.8	21.3	669	7	AQ035815	AQ035815	RPCT11-10
c 695	193.2	21.3	577	1	AV732057	AV732057	AV732057	c 768	192.8	21.3	746	5	BE632972	BE632972	UI-H-DPO-
c 696	193.2	21.3	579	8	AO546539	AO546539	CITBI-EI-	c 769	192.8	21.3	1007	1	AL544410	AL544410	full-leng
c 697	193.2	21.3	589	2	AM162555	AM162555	au77d06.x	c 770	192.8	21.3	1176	3	CR612626	CR612626	
c 698	193.2	21.3	594	5	BQ2772418	BQ2772418	lj98g01.x	c 771	192.6	21.2	346	5	BM991496	BM991496	
c 699	193.2	21.3	604	8	A2517781	A2517781	RPCT-11-1	c 772	192.6	21.2	370	5	BQ711408	BQ711408	AGENCOURT
c 700	193.2	21.3	638	4	BG427437	BG427437	602499161	c 773	192.6	21.2	420	1	A1049999	A1049999	an22a12.x
c 701	193.2	21.3	647	5	BK502809	BK502809	DKE2p779C	c 774	192.6	21.2	519	8	AO538500	AO538500	RPCT-11-3
c 702	193.2	21.3	658	7	H80463	H80463	y075b05.r1	c 775	192.6	21.2	546	5	BU899282	BU899282	
c 703	193.2	21.3	661	1	AV730440	AV730440	Homo sapi	c 776	192.6	21.2	579	1	AUI44608	AUI44608	
c 704	193.2	21.3	681	9	AG015022	AG015022	Homo sapi	c 777	192.6	21.2	582	5	BP250579	BP250579	
c 705	193.2	21.3	714	6	CD366358	CD366358	UI-H-FT1-	c 778	192.6	21.2	628	6	CA036131	CA036131	
c 706	193.2	21.3	767	1	AV700498	AV700498	mcE82h06.	c 779	192.6	21.2	639	9	AG080004	AG080004	Par tregl
c 707	193.2	21.3	781	8	BZ771947	BZ771947	WMADL64TF	c 780	192.6	21.2	655	9	AG080004	AG080004	
c 708	193.2	21.3	799	8	BZ610948	BZ610948	HS_3118_B	c 781	192.6	21.2	656	9	AG035209	AG035209	
c 709	193.2	21.3	888	5	BU162525	BU162525	AGENCOURT	c 782	192.6	21.2	658	8	AQ039450	AQ039450	
c 710	193.2	21.3	900	5	BU957335	BU957335	AGENCOURT	c 783	192.6	21.2	668	7	CK003906	CK003906	
c 711	193.2	21.3	917	5	BU963586	BU963586	AGENCOURT	c 784	192.6	21.2	688	5	BQ652218	BQ652218	
c 712	193.2	21.3	2110	3	BC012538	BC012538	Homo sapi	c 785	192.6	21.2	695	5	BU629128	BU629128	UI-H-FL0-
c 713	193.2	21.3	298	1	AA228979	AA228979	nc50a06.x	c 786	192.6	21.2	698	6	CA306826	CA306826	UI-H-FT1-
c 714	193.2	21.3	311	5	BU603673	BU603673	AGENCOURT	c 787	192.6	21.2	716	5	BM969125	BM969125	UI-CF-ENO
c 715	193.2	21.3	324	2	AM085626	AM085626	h04e01.x	c 788	192.6	21.2	718	2	BE883957	BE883957	601505473
c 716	193.2	21.3	354	7	NE5456	NE5456	y448e04.b1	c 789	192.6	21.2	756	5	EX341284	EX341284	
c 717	193.2	21.3	363	1	AA704393	AA704393	z18bh04.b	c 790	192.6	21.2	803	6	CB962282	CB962282	
c 718	193.2	21.3	374	4	BI492613	BI492613	df26g09.w	c 791	192.6	21.2	901	5	BQ230657	BQ230657	
c 719	193.2	21.3	375	2	AM021674	AM021674	df26g09.y	c 792	192.6	21.2	941	6	CD518779	CD518779	
c 720	193.2	21.3	382	1	AA566843	AA566843	nfl6f09.b	c 793	192.6	21.2	968	2	BF345228	BF345228	602018175
c 721	193.2	21.3	388	8	AQ212798	AQ212798	HS_3118_B	c 794	192.6	21.2	1055	5	BQ448298	BQ448298	
c 722	193.2	21.3	413	8	AQ664805	AQ664805	HS_5303_B	c 795	192.6	21.2	1113	5	EX444493	EX444493	
c 723	193.2	21.3	433	8	AM157128	AM157128	aub2g09.x	c 796	192.6	21.2	1163	3	HSMB0069	HSMB0069	
c 724	193.2	21.3	441	8	BM0074	BM0074	CIT-HSP-204	c 797	192.6	21.2	3341	3	CR749847	CR749847	Homo sapi
c 725	193.2	21.3	456	2	AM897556	AM897556	CM3-NN005	c 798	192.6	21.2	4667	3	BC038671	BC038671	
c 726	193.2	21.3	464	7	CR538317	CR538317	DKE2p459L	c 799	192.4	21.2	291	2	AA242234	AA242234	x024a05.x
c 727	193.2	21.3	480	7	CD679321	CD679321	h04e05.y	c 800	192.4	21.2	302	4	AG996738	AG996738	
c 728	193.2	21.3	536	8	AQ393821	AQ393821	CITBI-EI-	c 801	192.4	21.2	353	1	AA332320	AA332320	
c 729	193.2	21.3	541	1	AUI44497	AUI44497	AUI44497	c 802	192.4	21.2	356	8	AQ817094	AQ817094	HS_5553_A
c 730	193.2	21.3	552	7	CM264709	CM264709	170004244	c 803	192.4	21.2	379	1	A1911605	A1911605	wC86b01.x
c 731	193.2	21.3	553	5	BK484034	BK484034	DKE2p686A	c 804	192.4	21.2	387	6	CD708587	CD708587	
c 732	193.2	21.3	561	8	AQ387133	AQ387133	RPCT11-14	c 805	192.4	21.2	397	1	AI290008	AI290008	qw25g10.x
c 733	193.2	21.3	564	4	BI467196	BI467196	ic19c04.x	c 806	192.4	21.2	441	1	AI674873	AI674873	wc77f09.x
c 734	193.2	21.3	583	1	AL600288	AL600288	DKE2p313A	c 807	192.4	21.2	402	8	AQ527301	AQ527301	
c 735	193.2	21.3	619	7	CN414232	CN414232	170005830	c 808	192.4	21.2	406	8	BP1247	BP1247	CIT-HSP-216
c 736	193.2	21.3	629	8	AQ473496	AQ473496	CITBI-EI-	c 809	192.4	21.2	407	1	AA772906	AA772906	
c 737	193.2	21.3	642	8	BS9854	BS9854	CIT-HSP-345	c 810	192.4	21.2	435	1	AA122175	AA122175	zn29a05.b
c 738	193.2	21.3	648	8	BZ611349	BZ611349	WMAAO01TR	c 811	192.4	21.2	441	1	AI674873	AI674873	
c 739	193.2	21.3	663	4	BM742716	BM742716	K-EST0015	c 812	192.4	21.2	447	8	AQ484712	AQ484712	RPCT-11-2
c 740	193.2	21.3	681	8	BE772377	BE772377	mcv35905	c 813	192.4	21.2	467	4	BI438872	BI438872	ic27g01.x
c 741	193.2	21.3	698	9	AG119007	AG119007	Par tregl	c 814	192.4	21.2	477	7	CR738128	CR738128	
c 742	193.2	21.3	721	7	CR790056	CR790056	DKE2p459G	c 815	192.4	21.2	483	3	BP913232	BP913232	
c 743	193.2	21.3	809	7	CR232499	CR232499	ILLUMIGEN	c 816	192.4	21.2	490	2	BE138757	BE138757	
c 744	193.2	21.3	839	5	BK400315	BK400315	BK400315	c 817	192.4	21.2	498	5	BM959211	BM959211	UI-H-ED0-
c 745	193.2	21.3	874	5	BU187815	BU187815	AGENCOURT	c 818	192.4	21.2	504	8	BZ605467	BZ605467	
c 746	193.2	21.3	1890	3	CR599555	CR599555	full-leng	c 819	192.4	21.2	507	1	AA313025	AA313025	
c 747	193.2	21.3	2493	3	BC048794	BC048794	Homo sapi	c 820	192.4	21.2	518	4	BM090960	BM090960	
c 748	192.8	21.3	346	1	AA084148	AA084148	zn17c03.b	c 821	192.4	21.2	545	8	AQ268517	AQ268517	
c 749	192.8	21.3	371	7	CK000820	CK000820	AGENCOURT	c 822	192.4	21.2	551	4	BI438652	BI438652	
c 750	192.8	21.3	425	2	AM513569	AM513569	x086d00.x	c 823	192.4	21.2	556	1	AL597545	AL597545	DKE2p13H
c 751	192.8	21.3	430	2	AM513556	AM513556	x086d00.x	c 824	192.4	21.2	559	6	CA943760	CA943760	1r84f10.x
c 752	192.8	21.3	493	8	BH912810	BH912810	UP_354-9K	c 825	192.4	21.2	570	1	AUI49443	AUI49443	
c 753	192.8	21.3	507	5	BQ787605	BQ787605	im13b03.x	c 826	192.4	21.2	571	8	AQ381323	AQ381323	RPCT11-13
c 754	192.8	21.3	512	2	AM473541	AM473541	hb05f03.x	c 827	192.4	21.2	580	7	CK904663	CK904663	

C 828	192.4	21.2	585	1	AT571894	AT571894	tc20h06.x	901	192.2	21.2	716	9	AG185992	AG185992	Pan t1rog1
829	192.4	21.2	606	5	BO778458	BO778458	1131d07.x	902	192.2	21.2	733	6	CA429976	CA429976	UI-H-EZ0-
830	192.4	21.2	607	5	BX508704	BX508704	DKF2p686E	903	192.2	21.2	734	7	CA415430	CA415430	UI-H-EZ0-
831	192.4	21.2	617	5	BO632031	BO632031	1121e05.x	C 904	192.2	21.2	751	7	CN409704	CN409704	170005999
832	192.4	21.2	618	7	CN264754	CN264754	170004244	905	192.2	21.2	775	5	BX351849	BX351849	
C 833	192.4	21.2	619	5	BX505458	BX505458	DKF2p686E	906	192.2	21.2	783	8	AO537377	AO537377	RPCT-11-3
C 834	192.4	21.2	621	5	BO883117	BO883117	AGENCOURT	907	192.2	21.2	787	5	BM999347	BM999347	UI-H-DP0-
C 835	192.4	21.2	621	7	CN263879	CN263879	170004241	C 908	192.2	21.2	807	5	BU903326	BU903326	AGENCOURT
C 836	192.4	21.2	632	7	BO045015	BO045015	UI-H-EU0-	C 909	192.2	21.2	904	5	BU168982	BU168982	AGENCOURT
837	192.4	21.2	652	9	AG087320	AG087320	Pan t1rog1	C 910	192.2	21.2	1034	5	BU188260	BU188260	UI-H-EZ0-
C 838	192.4	21.2	654	1	AU117926	AU117926	AG117926	C 911	192.2	21.2	1844	3	CR619042	CR619042	full-1eng
C 839	192.4	21.2	656	6	CA420015	CA420015	UI-H-FH0-	C 912	192.2	21.2	1864	3	CR613224	CR613224	full-1eng
840	192.4	21.2	665	7	CN277676	CN277676	170006001	C 913	192.2	21.2	1884	3	CR594104	CR594104	full-1eng
841	192.4	21.2	668	9	AG169531	AG169531	Pan t1rog1	C 914	192.2	21.2	1886	3	CR625365	CR625365	full-1eng
842	192.4	21.2	684	4	BG333118	BG333118	602430809	C 915	192.2	21.2	1909	3	CR597717	CR597717	full-1eng
843	192.4	21.2	709	6	CD237100	CD237100	FNPAGC09	C 916	192.2	21.2	1916	3	CR622212	CR622212	full-1eng
C 844	192.4	21.2	712	6	CD246087	CD246087	AGENCOURT	C 917	192.2	21.2	2442	3	CR618116	CR618116	full-1eng
C 845	192.4	21.2	721	6	CD364665	CD364665	UI-H-FT2-	C 918	192	21.2	309	1	AA847341	AA847341	
C 846	192.4	21.2	722	7	CN263776	CN263776	170004241	C 919	192	21.2	343	1	AA636077	AA636077	
C 847	192.4	21.2	737	5	BX504515	BX504515	DKF2p686E	C 920	192	21.2	346	6	CD357102	CD357102	
C 848	192.4	21.2	745	9	AG085464	AG085464	Pan t1rog1	C 921	192	21.2	353	5	BU929075	BU929075	
C 849	192.4	21.2	754	8	BZ605835	BZ605835	WHACW42TR	C 922	192	21.2	354	1	AI137687	AI137687	
C 850	192.4	21.2	778	6	CB985162	CB985162	AGENCOURT	C 923	192	21.2	354	2	AM182182	AM182182	
851	192.4	21.2	779	6	CA442904	CA442904	UI-H-DP0-	C 924	192	21.2	375	2	AW182182	AW182182	
852	192.4	21.2	795	7	CF595558	CF595558	AGENCOURT	C 925	192	21.2	381	2	BE045167	BE045167	
853	192.4	21.2	885	6	CD514239	CD514239	AGENCOURT	C 926	192	21.2	447	6	CA434025	CA434025	
854	192.4	21.2	888	7	CF456538	CF456538	AGENCOURT	C 927	192	21.2	447	8	AO058688	AO058688	
855	192.4	21.2	1104	5	BX358486	BX358486	BX358486	C 928	192	21.2	449	8	AO058688	AO058688	
C 856	192.4	21.2	1486	3	CR623651	CR623651	full-1eng	C 929	192	21.2	477	8	CA439033	CA439033	
C 857	192.4	21.2	3540	3	CR749327	CR749327	Homo sapi	C 930	192	21.2	526	7	CR556759	CR556759	
C 858	192.4	21.2	361	1	AA661583	AA661583	nu86c08.s	C 931	192	21.2	526	4	BP944736	BP944736	
C 859	192.2	21.2	377	1	AI452836	AI452836	tj21b06.x	C 932	192	21.2	533	7	T76991	T76991	
C 860	192.2	21.2	406	8	AO427676	AO427676	CITBI-EI-	C 933	192	21.2	538	8	AO417891	AO417891	
861	192.2	21.2	418	8	BE005811	BE005811	RC2-BN012	C 934	192	21.2	542	6	CD691103	CD691103	
C 862	192.2	21.2	420	8	AI497824	AI497824	hm89g10.x	C 935	192	21.2	546	1	AI188995	AI188995	
C 863	192.2	21.2	474	2	AA975779	AA975779	Oq47b12.s	C 936	192	21.2	546	8	BE603328	BE603328	
C 864	192.2	21.2	468	5	BX101540	BX101540	BX101540	C 937	192	21.2	550	5	BU768083	BU768083	
C 865	192.2	21.2	483	1	AA975779	AA975779	RC5-BT070	C 938	192	21.2	554	1	AL171338	AL171338	
866	192.2	21.2	484	8	AO535388	AO535388	RPCT-11-3	C 939	192	21.2	568	2	BE144554	BE144554	
C 867	192.2	21.2	483	4	BE455742	BE455742	601076903	C 940	192	21.2	568	2	BE144554	BE144554	
C 868	192.2	21.2	493	8	BE455742	BE455742	RPCT-11-3	C 941	192	21.2	580	4	BE144554	BE144554	
C 869	192.2	21.2	499	8	AO539985	AO539985	RPCT-11-3	C 942	192	21.2	598	2	BE144554	BE144554	
C 870	192.2	21.2	517	8	AO436199	AO436199	RPCT-11-3	C 943	192	21.2	614	2	AW151824	AW151824	
C 871	192.2	21.2	518	1	AI573198	AI573198	t170909.x	C 944	192	21.2	620	1	AV171906	AV171906	
C 872	192.2	21.2	526	6	CA439937	CA439937	UI-H-DI0-	C 945	192	21.2	620	2	AM960129	AM960129	
C 873	192.2	21.2	526	6	CA439937	CA439937	UI-H-DI0-	C 946	192	21.2	621	8	AO550760	AO550760	
C 874	192.2	21.2	534	5	BX502385	BX502385	DKF2p779M	C 947	192	21.2	621	8	BM991115	BM991115	
C 875	192.2	21.2	564	8	AO006837	AO006837	CIT-HSP-2	C 948	192	21.2	665	5	BX508823	BX508823	
C 876	192.2	21.2	564	8	BM633248	BM633248	1927610.x	C 949	192	21.2	685	9	AG176669	AG176669	
C 877	192.2	21.2	569	4	BM633667	BM633667	1927610.x	C 950	192	21.2	698	9	CD239400	CD239400	
C 878	192.2	21.2	577	8	AO483308	AO483308	RPCT-11-2	C 951	192	21.2	733	7	CR742950	CR742950	
C 879	192.2	21.2	584	5	BP205616	BP205616	RPCT-11-2	C 952	192	21.2	747	7	CR742950	CR742950	
C 880	192.2	21.2	591	6	CB055261	CB055261	NISC gm08	C 953	192	21.2	801	4	BC547968	BC547968	
C 881	192.2	21.2	591	2	BE276686	BE276686	601144784	C 954	192	21.2	874	3	BC032901	BC032901	
C 882	192.2	21.2	604	4	BM740671	BM740671	K-E8T0012	C 955	192	21.2	894	5	BX430934	BX430934	
883	192.2	21.2	606	6	CA423390	CA423390	UI-H-FL0-	C 956	192	21.2	932	5	BO959144	BO959144	
884	192.2	21.2	609	8	AO540554	AO540554	RPCT-11-3	C 957	192	21.2	932	5	BO959144	BO959144	
885	192.2	21.2	612	7	CK818280	CK818280	1c23f12.y	C 958	192	21.2	970	4	BE118544	BE118544	
C 886	192.2	21.2	629	7	CN360036	CN360036	170005318	C 959	192	21.2	1054	3	CR605219	CR605219	
C 887	192.2	21.2	630	2	AM957739	AM957739	EST169809	C 960	192	21.2	1217	3	CR613023	CR613023	
C 888	192.2	21.2	636	8	AO266645	AO266645	RPCT-11-74	C 961	192	21.2	1647	3	CR620185	CR620185	
C 889	192.2	21.2	660	5	BU184851	BU184851	AGENCOURT	C 962	192	21.2	2352	1	AA503142	AA503142	
C 890	192.2	21.2	683	5	BU184851	BU184851	UI-CR-ECL	C 963	191.8	21.1	330	8	AA503142	AA503142	
C 891	192.2	21.2	689	5	AG105245	AG105245	Pan t1rog1	C 964	191.8	21.1	396	5	BM988047	BM988047	
C 892	192.2	21.2	690	8	AO375664	AO375664	RPCT-11-14	C 965	191.8	21.1	432	8	AO047116	AO047116	
893	192.2	21.2	692	8	CA439730	CA439730	UI-H-DI0-	C 966	191.8	21.1	432	8	AO047116	AO047116	
894	192.2	21.2	695	6	CA447335	CA447335	UI-H-EI0-	C 967	191.8	21.1	459	2	BF448553	BF448553	
895	192.2	21.2	697	6	BI256839	BI256839	602974924	C 968	191.8	21.1	459	8	AO150790	AO150790	
C 896	192.2	21.2	702	4	BO183748	BO183748	UI-H-EU0-	C 969	191.8	21.1	501	8	AO588985	AO588985	
C 897	192.2	21.2	708	5	BU624395	BU624395	UI-H-FG1-	C 970	191.8	21.1	507	7	CR558360	CR558360	
C 898	192.2	21.2	711	5	BM999347	BM999347	UI-H-DP0-	C 971	191.8	21.1	512	5	BO029024	BO029024	
C 899	192.2	21.2	714	7	CN409711	CN409711	170005332	C 972	191.8	21.1	538	5	BU584984	BU584984	
C 900	192.2	21.2	715	2	BE742024	BE742024	601594513	C 973	191.8	21.1	563	1	AV720143	AV720143	

C 974	191.8	21.1	573	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1047	191.4	21.1	445	1	AA426451
C 975	191.8	21.1	609	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1048	191.4	21.1	456	7	CR746133
C 976	191.8	21.1	614	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1049	191.4	21.1	460	2	BE151469
C 977	191.8	21.1	638	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1050	191.4	21.1	469	5	BQ029488
C 978	191.8	21.1	644	9	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1051	191.4	21.1	470	1	AA568303
C 979	191.8	21.1	674	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1052	191.4	21.1	492	8	AQ480120
C 980	191.8	21.1	678	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1053	191.4	21.1	493	4	BM509931
C 981	191.8	21.1	686	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1054	191.4	21.1	504	4	BM264427
C 982	191.8	21.1	693	9	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1055	191.4	21.1	505	8	AQ052041
C 983	191.8	21.1	715	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1056	191.4	21.1	514	8	AQ002001
C 984	191.8	21.1	714	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1057	191.4	21.1	555	8	B82781
C 985	191.8	21.1	735	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1058	191.4	21.1	556	8	AQ0372425
C 986	191.8	21.1	750	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1059	191.4	21.1	570	5	BK500944
C 987	191.8	21.1	759	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1060	191.4	21.1	577	5	BP152045
C 988	191.8	21.1	836	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1061	191.4	21.1	580	5	BQ638992
C 989	191.8	21.1	873	6	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1062	191.4	21.1	581	5	BK036780
C 990	191.8	21.1	882	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1063	191.4	21.1	619	5	BQ777329
C 991	191.8	21.1	884	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1064	191.4	21.1	636	5	AV731385
C 992	191.8	21.1	911	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1065	191.4	21.1	638	6	CB151593
C 993	191.8	21.1	1057	4	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1066	191.4	21.1	639	5	BM992802
C 994	191.8	21.1	1077	3	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1067	191.4	21.1	655	6	CA417141
C 995	191.8	21.1	1146	4	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1068	191.4	21.1	656	9	AG058334
C 996	191.8	21.1	1226	3	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1069	191.4	21.1	656	9	AG118439
C 997	191.8	21.1	2213	3	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1070	191.4	21.1	712	5	BQ574095
C 998	191.6	21.1	311	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1071	191.4	21.1	720	4	BG700708
C 999	191.6	21.1	329	7	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1072	191.4	21.1	729	5	BQ231303
C1000	191.6	21.1	334	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1073	191.4	21.1	736	7	CN278157
C1001	191.6	21.1	350	7	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1074	191.4	21.1	746	4	BE882869
C1002	191.6	21.1	379	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1075	191.4	21.1	747	4	BG358523
C1003	191.6	21.1	404	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1076	191.4	21.1	784	9	CL423322
C1004	191.6	21.1	430	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1077	191.4	21.1	792	8	B2772915
C1005	191.6	21.1	451	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1078	191.4	21.1	875	4	BG503933
C1006	191.6	21.1	472	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1079	191.4	21.1	934	5	BQ680709
C1007	191.6	21.1	479	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1080	191.4	21.1	946	5	BE680232
C1008	191.6	21.1	494	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1081	191.4	21.1	965	5	BU944090
C1009	191.6	21.1	500	9	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1082	191.4	21.1	1078	1	AL537956
C1010	191.6	21.1	505	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1083	191.4	21.1	1089	5	BK444303
C1011	191.6	21.1	510	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1084	191.4	21.1	1155	4	BM558132
C1012	191.6	21.1	518	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1085	191.4	21.1	1357	3	CR623688
C1013	191.6	21.1	524	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1086	191.4	21.1	1388	3	AY203942
C1014	191.6	21.1	532	4	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1087	191.4	21.1	1658	3	CR625865
C1015	191.6	21.1	566	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1088	191.4	21.1	1687	3	CR620860
C1016	191.6	21.1	573	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1089	191.4	21.1	2442	3	BQ633247
C1017	191.6	21.1	582	7	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1090	191.4	21.1	2821	3	BM603247
C1018	191.6	21.1	613	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1091	191.4	21.1	8213	3	BSM809146
C1019	191.6	21.1	613	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1092	191.2	21.1	318	5	BU536535
C1020	191.6	21.1	649	9	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1093	191.2	21.1	319	7	BE530611
C1021	191.6	21.1	656	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1094	191.2	21.1	335	7	CN420204
C1022	191.6	21.1	674	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1095	191.2	21.1	340	1	AA199582
C1023	191.6	21.1	678	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1096	191.2	21.1	366	1	AI503673
C1024	191.6	21.1	678	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1097	191.2	21.1	393	1	AV703042
C1025	191.6	21.1	679	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1098	191.2	21.1	409	8	AO068809
C1026	191.6	21.1	680	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1099	191.2	21.1	432	8	AO039841
C1027	191.6	21.1	702	9	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1100	191.2	21.1	443	8	AO117380
C1028	191.6	21.1	831	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1101	191.2	21.1	444	8	AO114248
C1029	191.6	21.1	856	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1102	191.2	21.1	449	8	AO057953
C1030	191.6	21.1	891	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1103	191.2	21.1	468	5	BQ559970
C1031	191.6	21.1	924	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1104	191.2	21.1	482	8	AO226590
C1032	191.6	21.1	945	5	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1105	191.2	21.1	493	5	BU930264
C1033	191.6	21.1	1250	3	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1106	191.2	21.1	497	8	AO140042
C1034	191.6	21.1	2125	3	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1107	191.2	21.1	509	8	AO236686
C1035	191.4	21.1	343	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1108	191.2	21.1	512	8	AO412029
C1036	191.4	21.1	343	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1109	191.2	21.1	518	5	BU077884
C1037	191.4	21.1	345	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1110	191.2	21.1	526	7	CN275115
C1038	191.4	21.1	384	2	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1111	191.2	21.1	551	6	CA429701
C1039	191.4	21.1	389	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1112	191.2	21.1	552	6	AO599255
C1040	191.4	21.1	407	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1113	191.2	21.1	553	8	AO356363
C1041	191.4	21.1	416	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1114	191.2	21.1	574	1	AO147781
C1042	191.4	21.1	432	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1115	191.2	21.1	574	5	AO898821
C1043	191.4	21.1	434	8	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1116	191.2	21.1	607	8	AO487852
C1044	191.4	21.1	435	7	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1117	191.2	21.1	610	5	BU178885
C1045	191.4	21.1	437	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1118	191.2	21.1	621	8	AO629567
C1046	191.4	21.1	437	1	BM92855	UI-H-DT0-	BM92855	UI-H-DT0-	C1119	191.2	21.1	648	5	BK505461

c1120	191.2	21.1	678	6	CA422648	UI-H-FIO-	c1193	190.8	21.0	583	4	BI467327	IC22h11.x
c1121	191.2	21.1	694	4	BM686366	UI-B-CRO-	c1194	190.8	21.0	584	5	BU078874	Im71d06.x
c1122	191.2	21.1	705	1	AV732420	AV732420	c1195	190.8	21.0	585	2	BP218253	601885589
c1123	191.2	21.1	729	1	AV704541	AV704541	c1196	190.8	21.0	648	5	BQ894783	AGENCOURT
c1124	191.2	21.1	779	8	AO630496	AO630496	c1197	190.8	21.0	657	5	BO626531	UI-H-FIO-
c1125	191.2	21.1	851	2	BF346854	602021664	c1198	190.8	21.0	658	9	AG183592	Pan tCrog1
c1126	191.2	21.1	1073	8	B2601227	WHADC89TR	c1199	190.8	21.0	665	8	A2520516	RCPT-11-3
c1127	191.2	21.1	1074	3	CR620015	Full-1eng	c1200	190.8	21.0	667	8	B2602960	WHAB156TR
c1128	191.2	21.1	1074	3	CR620015	Full-1eng	c1201	190.8	21.0	670	9	AG051703	Pan tCrog1
c1129	191.2	21.1	1074	3	CR620015	Full-1eng	c1202	190.8	21.0	677	9	AG051703	Pan tCrog1
c1130	191.2	21.1	1074	3	CR620015	Full-1eng	c1203	190.8	21.0	677	9	AG051703	Pan tCrog1
c1131	191.2	21.1	1074	3	CR620015	Full-1eng	c1204	190.8	21.0	680	5	AG176489	Pan tCrog1
c1132	191.2	21.1	1074	3	CR620015	Full-1eng	c1205	190.8	21.0	682	5	BM994908	UI-H-DIO-
c1133	191.2	21.1	1074	3	CR620015	Full-1eng	c1206	190.8	21.0	709	1	AV649109	AV649109
c1134	191.2	21.1	1074	3	CR620015	Full-1eng	c1207	190.8	21.0	714	8	AO878839	HS 3144 B
c1135	191.2	21.1	1074	3	CR620015	Full-1eng	c1208	190.8	21.0	716	5	BU617628	UI-H-DIO-
c1136	191.2	21.1	1074	3	CR620015	Full-1eng	c1209	190.8	21.0	720	4	BM707416	BM707416
c1137	191.2	21.1	1074	3	CR620015	Full-1eng	c1210	190.8	21.0	727	5	BM990571	UI-H-DIO-
c1138	191.2	21.1	1074	3	CR620015	Full-1eng	c1211	190.8	21.0	727	6	CA442999	CA442999
c1139	191.2	21.1	1074	3	CR620015	Full-1eng	c1212	190.8	21.0	737	6	BS904397	BS904397
c1140	191.2	21.1	1074	3	CR620015	Full-1eng	c1213	190.8	21.0	748	1	CA417973	CA417973
c1141	191.2	21.1	1074	3	CR620015	Full-1eng	c1214	190.8	21.0	774	6	AO175753	AO175753
c1142	191.2	21.1	1074	3	CR620015	Full-1eng	c1215	190.8	21.0	904	5	BO707416	BO707416
c1143	191.2	21.1	1074	3	CR620015	Full-1eng	c1216	190.8	21.0	913	5	BM390441	BM390441
c1144	191.2	21.1	1074	3	CR620015	Full-1eng	c1217	190.8	21.0	932	4	BM390441	BM390441
c1145	191.2	21.1	1074	3	CR620015	Full-1eng	c1218	190.8	21.0	1023	1	AL523272	AL523272
c1146	191.2	21.1	1074	3	CR620015	Full-1eng	c1219	190.8	21.0	1145	4	CR612064	CR612064
c1147	191.2	21.1	1074	3	CR620015	Full-1eng	c1220	190.8	21.0	1471	3	CR612064	CR612064
c1148	191.2	21.1	1074	3	CR620015	Full-1eng	c1221	190.8	21.0	1542	3	CR612064	CR612064
c1149	191.2	21.1	1074	3	CR620015	Full-1eng	c1222	190.8	21.0	1619	3	HSMB804364	HSMB804364
c1150	191.2	21.1	1074	3	CR620015	Full-1eng	c1223	190.8	21.0	1659	3	CR602249	CR602249
c1151	191.2	21.1	1074	3	CR620015	Full-1eng	c1224	190.8	21.0	2504	3	HSMB802853	HSMB802853
c1152	191.2	21.1	1074	3	CR620015	Full-1eng	c1225	190.8	21.0	2782	3	CR621797	CR621797
c1153	191.2	21.1	1074	3	CR620015	Full-1eng	c1226	190.8	21.0	3127	3	AF447879	AF447879
c1154	191.2	21.1	1074	3	CR620015	Full-1eng	c1227	190.8	21.0	330	5	BU566680	BU566680
c1155	191.2	21.1	1074	3	CR620015	Full-1eng	c1228	190.8	21.0	381	2	AW117860	AW117860
c1156	191.2	21.1	1074	3	CR620015	Full-1eng	c1229	190.8	21.0	420	8	BS599910	BS599910
c1157	191.2	21.1	1074	3	CR620015	Full-1eng	c1230	190.8	21.0	422	2	BE005805	BE005805
c1158	191.2	21.1	1074	3	CR620015	Full-1eng	c1231	190.8	21.0	430	2	AW627747	AW627747
c1159	191.2	21.1	1074	3	CR620015	Full-1eng	c1232	190.8	21.0	432	2	AW971320	AW971320
c1160	191.2	21.1	1074	3	CR620015	Full-1eng	c1233	190.8	21.0	438	7	CR739570	CR739570
c1161	191.2	21.1	1074	3	CR620015	Full-1eng	c1234	190.8	21.0	444	8	AO219325	AO219325
c1162	191.2	21.1	1074	3	CR620015	Full-1eng	c1235	190.8	21.0	461	2	BS089817	BS089817
c1163	191.2	21.1	1074	3	CR620015	Full-1eng	c1236	190.8	21.0	472	1	AA572983	AA572983
c1164	191.2	21.1	1074	3	CR620015	Full-1eng	c1237	190.8	21.0	476	7	N67313	N67313
c1165	191.2	21.1	1074	3	CR620015	Full-1eng	c1238	190.8	21.0	486	5	EA496624	EA496624
c1166	191.2	21.1	1074	3	CR620015	Full-1eng	c1239	190.8	21.0	487	7	CN276954	CN276954
c1167	191.2	21.1	1074	3	CR620015	Full-1eng	c1240	190.8	21.0	486	5	EA496624	EA496624
c1168	191.2	21.1	1074	3	CR620015	Full-1eng	c1241	190.8	21.0	487	7	CN276954	CN276954
c1169	191.2	21.1	1074	3	CR620015	Full-1eng	c1242	190.8	21.0	487	7	CN276954	CN276954
c1170	191.2	21.1	1074	3	CR620015	Full-1eng	c1243	190.8	21.0	487	7	CN276954	CN276954
c1171	191.2	21.1	1074	3	CR620015	Full-1eng	c1244	190.8	21.0	487	7	CN276954	CN276954
c1172	191.2	21.1	1074	3	CR620015	Full-1eng	c1245	190.8	21.0	487	7	CN276954	CN276954
c1173	191.2	21.1	1074	3	CR620015	Full-1eng	c1246	190.8	21.0	487	7	CN276954	CN276954
c1174	191.2	21.1	1074	3	CR620015	Full-1eng	c1247	190.8	21.0	487	7	CN276954	CN276954
c1175	190.8	21.0	298	2	BM150589	BM150589	c1248	190.6	21.0	544	2	AO506882	AO506882
c1176	190.8	21.0	344	2	BM150589	BM150589	c1249	190.6	21.0	552	1	AI921706	AI921706
c1177	190.8	21.0	346	1	BM150589	BM150589	c1250	190.6	21.0	571	8	AO484348	AO484348
c1178	190.8	21.0	402	1	BM150589	BM150589	c1251	190.6	21.0	571	8	AO484348	AO484348
c1179	190.8	21.0	406	7	BM150589	BM150589	c1252	190.6	21.0	590	8	AO313925	AO313925
c1180	190.8	21.0	418	1	BM150589	BM150589	c1253	190.6	21.0	606	8	BS4647	BS4647
c1181	190.8	21.0	437	7	BM150589	BM150589	c1254	190.6	21.0	616	5	EA483542	EA483542
c1182	190.8	21.0	447	1	BM150589	BM150589	c1255	190.6	21.0	629	5	BS057857	BS057857
c1183	190.8	21.0	477	1	BM150589	BM150589	c1256	190.6	21.0	638	6	CB055260	CB055260
c1184	190.8	21.0	489	6	BM150589	BM150589	c1257	190.6	21.0	644	7	CV368474	CV368474
c1185	190.8	21.0	494	1	BM150589	BM150589	c1258	190.6	21.0	651	6	CA778069	CA778069
c1186	190.8	21.0	500	6	BM150589	BM150589	c1259	190.6	21.0	659	2	AW929295	AW929295
c1187	190.8	21.0	516	8	BM150589	BM150589	c1260	190.6	21.0	669	8	AO322876	AO322876
c1188	190.8	21.0	517	1	BM150589	BM150589	c1261	190.6	21.0	674	9	AG123283	AG123283
c1189	190.8	21.0	522	1	BM150589	BM150589	c1262	190.6	21.0	680	5	CA397305	CA397305
c1190	190.8	21.0	544	4	BM150589	BM150589	c1263	190.6	21.0	677	6	BO773564	BO773564
c1191	190.8	21.0	574	4	BM150589	BM150589	c1264	190.6	21.0	693	8	AO412920	AO412920
c1192	190.8	21.0	576	6	CA427630	UI-H-EDO-	c1265	190.6	21.0	711	6	CA445780	UI-H-EDO-

C1266	190.6	21.0	723	6	CA431699	UI-H-DF0-	1339	190.2	21.0	469	5	BU660220	c157e10.z
1267	190.6	21.0	727	5	BU561234	AGENCYCOURT	C1340	190.2	21.0	470	8	AQ226326	HS_2010_A
C1268	190.6	21.0	753	1	AL691690	DKFZD313B	C1341	190.2	21.0	477	8	AQ632842	RPCT-11-4
1269	190.6	21.0	801	5	BQ214885	AGENCYCOURT	C1342	190.2	21.0	490	8	AQ432147	HS_5050_A
1270	190.6	21.0	833	4	BG286471	AGENCYCOURT	C1343	190.2	21.0	494	2	BE808768	QVI-BT063
1271	190.6	21.0	882	5	BQ228201	AGENCYCOURT	C1344	190.2	21.0	498	7	CR787110	DKFZP49K
1272	190.6	21.0	890	4	BG163987	602343185	C1345	190.2	21.0	520	6	CA964754	CA964754
1273	190.6	21.0	895	2	BF674823	602137982	C1346	190.2	21.0	525	8	AQ086123	RPCT11-54
1274	190.6	21.0	949	1	AL568770	AL568770	C1347	190.2	21.0	528	8	BS5695	CIT-HSP-200
1275	190.6	21.0	1065	4	BM454948	AGENCYCOURT	C1348	190.2	21.0	552	4	BI223275	602941310
1276	190.6	21.0	1088	4	BM477840	AGENCYCOURT	C1349	190.2	21.0	564	5	BU860291	AGENCYCOURT
C1277	190.6	21.0	5108	3	HSMB02883	AL512743	C1350	190.2	21.0	566	5	BU957747	AGENCYCOURT
C1278	190.6	21.0	8421	3	HSMB08381	BM454948	C1351	190.2	21.0	570	8	AQ018599	CIT-HSP-2
1279	190.4	21.0	398	1	AA857377	od83g11.s	C1352	190.2	21.0	574	8	AQ050760	RPCT-11-2
C1280	190.4	21.0	410	1	AL674290	AL674290	C1353	190.2	21.0	577	8	BI4093	A_864HS_TP
C1281	190.4	21.0	416	8	AQ140695	HS_3112.A	C1354	190.2	21.0	589	8	AQ041600	CIT-HSP-2
1282	190.4	21.0	420	1	AA167656	zq38f01.s	C1355	190.2	21.0	601	5	BSX04170	DKFZP686P
C1283	190.4	21.0	448	1	AL1471481	ta20g07.x	C1356	190.2	21.0	607	8	BZ603705	WHADEP21TR
C1284	190.4	21.0	453	1	AL144830	cr15f01.x	C1357	190.2	21.0	607	9	AG018337	W27084
1285	190.4	21.0	454	4	BG006718	QV4-GN012	C1358	190.2	21.0	613	7	W27084	20a9_Human
C1286	190.4	21.0	481	1	AL704739	DKFZP686I	C1359	190.2	21.0	625	9	AG018336	Hom0_sapi
C1287	190.4	21.0	487	1	AA618531	np38a03.s	C1360	190.2	21.0	637	8	AQ423458	CITBI-EI-
C1288	190.4	21.0	487	8	AQ425255	CITBI-EI-	C1361	190.2	21.0	639	6	CA308017	UI-H-PT1-
C1289	190.4	21.0	492	8	AQ198722	RPCT11-59	C1362	190.2	21.0	663	1	AL709338	DKFZP686F
1290	190.4	21.0	494	8	AQ392572	CITBI-EI-	C1363	190.2	21.0	666	9	AG040280	Pan trogl
1291	190.4	21.0	502	8	AQ391359	CITBI-EI-	C1364	190.2	21.0	666	9	AG182057	Pan trogl
C1292	190.4	21.0	524	8	BZ611490	WHACSO6TP	C1365	190.2	21.0	667	9	AG165154	Pan trogl
1293	190.4	21.0	552	8	AQ377725	RPCT11-15	C1366	190.2	21.0	672	1	AV648612	AV648612
C1294	190.4	21.0	556	8	AQ000806	HS_5299_A	C1367	190.2	21.0	687	1	AL174827	HA2550_Hu
C1295	190.4	21.0	569	8	AZ520604	RPCT-11-3	C1368	190.2	21.0	695	9	AG178603	Pan trogl
1296	190.4	21.0	623	5	BP336447	BP336447	C1369	190.2	21.0	699	7	CR789789	DKFZP495E
1297	190.4	21.0	629	5	BO7072384	im46B06.x	C1370	190.2	21.0	706	9	AG133042	Pan trogl
C1298	190.4	21.0	629	5	BO786682	il50a07.x	C1371	190.2	21.0	709	8	AO632003	RPCT-11-4
C1299	190.4	21.0	655	9	AG134408	Pan trogl	C1372	190.2	21.0	709	9	AG143216	Pan trogl
C1300	190.4	21.0	657	8	AQ624700	CITBI-EI-	C1373	190.2	21.0	721	9	AG085756	Pan trogl
1301	190.4	21.0	664	9	AG0505105	Pan trogl	C1374	190.2	21.0	828	8	BZ599498	WHACAO1TR
C1302	190.4	21.0	667	9	AG159164	Pan trogl	C1375	190.2	21.0	871	4	BI856069	603383457
1303	190.4	21.0	668	9	AG146787	Pan trogl	C1376	190.2	21.0	898	5	BU181297	AGENCYCOURT
1304	190.4	21.0	679	9	AG159116	Pan trogl	C1377	190.2	21.0	1049	5	AL572160	AL572160
1305	190.4	21.0	726	9	AG164176	Pan trogl	C1378	190.2	21.0	1080	5	BQ213854	AGENCYCOURT
C1306	190.4	21.0	731	4	BM682595	UI-H-ED1-	C1379	190.2	21.0	1170	3	BC017436	Hom0_sapi
1307	190.4	21.0	732	6	CA427215	UI-H-DF0-	C1380	190.2	21.0	1805	3	CR621123	full-Leng
C1308	190.4	21.0	741	7	CR704807	CR748203	C1381	190.2	21.0	1888	3	BC037885	Hom0_sapi
C1309	190.4	21.0	759	5	BO014487	UI-H-ED1-	C1382	190.2	21.0	385	8	AQ278103	CITBI-EI-
1310	190.4	21.0	769	5	BO710315	AGENCYCOURT	C1383	190.2	21.0	390	9	AG192505	Pan trogl
C1311	190.4	21.0	829	6	CB308284	AGENCYCOURT	C1384	190.2	21.0	412	1	AL7735609	AL7735609
1312	190.4	21.0	861	8	AQ897084	HS_3153_A	C1385	190.2	21.0	414	4	BG112362	602281927
1313	190.4	21.0	877	5	BQ953835	AGENCYCOURT	C1386	190.2	21.0	420	7	CN277619	170006001
C1314	190.4	21.0	911	6	CD520000	AGENCYCOURT	C1387	190.2	21.0	424	4	BI324902	ic19b08.x
1315	190.4	21.0	938	9	CL423157	RP11-883M	C1388	190.2	21.0	431	1	AA015948	2630c12.B
C1316	190.4	21.0	947	5	BO707946	AGENCYCOURT	C1389	190.2	21.0	439	2	AAW659462	h884g01.x
1317	190.4	21.0	954	2	BE618927	601472601	C1390	190.2	21.0	455	1	AA7748071	DK68609.s
1318	190.4	21.0	987	5	BK417024	BK417024	C1391	190.2	21.0	466	8	AQ382614	RPCT11-13
1319	190.4	21.0	1007	1	AL548632	AL548632	C1392	190.2	21.0	469	8	AQ029854	RPCT11-37
C1320	190.4	21.0	1122	1	AL525584	AGENCYCOURT	C1393	190.2	21.0	479	7	CN276493	170006001
C1321	190.4	21.0	1306	3	BC022398	Hom0_sapi	C1394	190.2	21.0	491	2	AAW659214	hC790005.x
C1322	190.4	21.0	4050	3	CR749265	Hom0_sapi	C1395	190.2	21.0	508	8	AQ418545	RPCT-11-2
C1323	190.4	21.0	4086	3	HSMB07683	Hom0_sapi	C1396	190.2	21.0	509	1	AL8155210	W472d06.x
C1324	190.4	21.0	4717	3	BC039267	Hom0_sapi	C1397	190.2	21.0	529	4	BG402924	602418727
C1325	190.4	21.0	7180	3	HSMB04869	Hom0_sapi	C1398	190.2	21.0	529	8	BI15895	346G12_TP.C
C1326	190.2	21.0	318	7	NS5076	YV43b07.B1	C1399	190.2	21.0	541	7	CN2653446	170004240
C1327	190.2	21.0	344	1	AL708108	AGENCYCOURT	C1400	190.2	21.0	543	5	BU947622	1055D06.x
C1328	190.2	21.0	356	1	AA349923	EST56987	C1401	190.2	21.0	573	3	BU173705	AGENCYCOURT
1329	190.2	21.0	389	1	AA084320	zn18b07.s	C1402	190.2	21.0	574	8	AQ820118	HS_5299_A
C1330	190.2	21.0	389	1	AL581006	c194a05.x	C1403	190.2	21.0	588	7	CN344468	170006000
C1331	190.2	21.0	408	1	AL362442	q936a03.x	C1404	190.2	21.0	598	4	BF977720	602148339
C1332	190.2	21.0	426	1	AL205783	q933a07.x	C1405	190.2	21.0	619	8	CA4545078	CITBI-EI-
1333	190.2	21.0	430	8	AQ270854	HS_2047_A	C1406	190.2	21.0	624	6	CA416290	UI-H-FE0-
1334	190.2	21.0	433	2	BE005743	RC7-BNO12	C1407	190.2	21.0	660	4	BG771029	602719285
1335	190.2	21.0	436	8	AQ062816	CIT-HSP-2	C1408	190.2	21.0	684	8	BZ603428	WHAHA707P
C1336	190.2	21.0	446	4	BM672913	UI-E-CQ0-	C1409	190.2	21.0	698	1	AV728560	AV728560
1337	190.2	21.0	453	8	AQ187593	HS_3132_A	C1410	190.2	21.0	699	1	AI905408	RC-BT091-
C1338	190.2	21.0	465	1	AA598889	ae37d09.B	C1411	190.2	21.0	707	6	CA449236	UI-H-ED0-

1412	1413	1414	1415	1416	1417	1418	1419	1420	1421	1422	1423	1424	1425	1426	1427	1428	1429	1430	1431	1432	1433	1434	1435	1436	1437	1438	1439	1440	1441	1442	1443	1444	1445	1446	1447	1448	1449	1450	1451	1452	1453	1454	1455	1456	1457	1458	1459	1460	1461	1462	1463	1464	1465	1466	1467	1468	1469	1470	1471	1472	1473	1474	1475	1476	1477	1478	1479	1480	1481	1482	1483	1484	1485	1486	1487	1488	1489	1490	1491	1492	1493	1494	1495	1496	1497	1498	1499	1500																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150	150

	LOCUS	BF915910/c	470 bp	mRNA	linear	EST 18-JAN-2001
	DEFINITION	IL3-UT0114-081200-366-E06 UT0114 Homo sapiens cDNA, mRNA sequence.				
	ACCESSION	BF915910				
	VERSION	BF915910.1	GI:12307368			
	KEYWORDS	EST.				
	SOURCE	Homo sapiens (human)				
	ORGANISM	Homo sapiens				
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	REFERENCE	1 (bases 1 to 470)				
	AUTHORS	Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Negai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goidman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.J.				
	TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags				
	JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
	MEDLINE	20202663				
	PUBMED	10737800				
	COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel.: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the PAPERP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l=IL3&t2=IL3-UT0114 081200-366-E06&t3=2000-12-08&t4=1) Seq primer: puc 18 forward High quality sequence stop: 455. Location/Qualifiers				
FEATURES	source	1..470				
		/organism="Homo sapiens"				
		/mol_type="mRNA"				
		/db_xref="taxon:9606"				
		/dev_stage="Adult"				
		/clone_lib="UT0114"				
		/note="Organ: uterine tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."				
ORIGIN						
	Query Match	51.8%; Score 470; DB 2; Length 470;				
	Best Local Similarity	100.0%; Pred. No. 5,4e-67;				
	Matches	470; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Gy	90	AGATACTGAGGGCAGGACCCCATATGGGAATGTACTCTCGCTTCACCTGCCT	149			
Dd	470	AGATTAACGTGAGGGCAGGACCCCATATGGGAATGTACTCTCGCTTCACCTGCCT	411			
Gy	150	GGTGTTCACAGTGGCTGTCTCTCTCTTGCCGAGAAGTGTCTTGGGTCAAGGACGCCA	209			
Dd	410	GGTGTTCACAGTGGCTGTCTCTCTCTTGCCGAGAAGTGTCTTGGGTCAAGGACGCCA	351			
Gy	210	GGAGGCTCACAGACTGCAGCCCTTTGTTACCGAGAGAACATTGGCAAGGTCCAGCGATG	269			
Dd	350	GGAGGCTCACAGACTGCAGCCCTTTGTTACCGAGAGAACATTGGCAAGGTCCAGCGATG	291			
Gy	270	GTCCGGAAGTCCACAACAAGACTGGCGGACAGGACGAGAGGGGAGACAGTTCTGTGTGCTTG	329			
Dd	299	GTCCGGAAGTCCACAACAAGACTGGCGGACAGGACGAGAGGGGAGACAGTTCTGTGTGCTTG	231			
Gy	330	GTTGGAACAGTAAAGAGGCTTTGGCCAGTCCAGAGTGGGGGGCGCAAATCCATTAAGAA	389			

Db	Query Match	Score	DB 2;	Length	470;
230	GTTCGACAGTGAAGGGCTCTTGGCCAGTCCAGGCTGGGGGGGGGCAAACTCCATTAAGAA	99.8%	Pred. No. 7.8e-67;	Indels 0;	Gaps 0;
390	CCAGAGGGTCTGGGGCCCGGCGCACAGATCATCTGCCAGCTCTTGTCTGTGGCCAGT	99.8%	Pred. No. 7.8e-67;	Indels 0;	Gaps 0;
170	CCAGAGGGTCTGGGGCCCGGCGCACAGATCATCTGCCAGCTCTTGTCTGTGGCCAGT	99.8%	Pred. No. 7.8e-67;	Indels 0;	Gaps 0;
450	GGAGTGGCACAGAGTGGGGCTTTGGCCAGTAAACACAGAGCTGGATTGGCTGGGG	99.8%	Pred. No. 7.8e-67;	Indels 0;	Gaps 0;
110	GGAGTGGCACAGAGTGGGGCTTTGGCCAGTAAACACAGAGCTGGATTGGCTGGGG	99.8%	Pred. No. 7.8e-67;	Indels 0;	Gaps 0;
510	CCATGGTCCCTGTCTAGGGCAGCAATCTCAACCTTCTCTCTCAGAC	99.8%	Pred. No. 7.8e-67;	Indels 0;	Gaps 0;
50	CCATGGTCCCTGTCTAGGGCAGCAATCTCAACCTTCTCTCTCAGAC	99.8%	Pred. No. 7.8e-67;	Indels 0;	Gaps 0;

[illegible]

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3032737"
/lab_host="RDH10B (T1 phage-resistant)"
/clone_lib="NTH MGC 184"
/note="Organ: Pooled Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccatctggccg); Site_2: SfiI (ggccctgcgcgc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyroid parathyroid, adrenal, cortex and pineal gland. 5' and 3'

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adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGGCGAGGGCCGACATG-dT(30)-BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

Query Match	51.4%	Score 466.4	DB 6	Length 792
Best Local Similarity	95.7%	Pred. No. 1.7e-66		
Matches 534, Conservative	0	Mismatches 16	Indels 8	Gaps 5

OY	210	GGAGGCTCAGACATCCACGCCCTTTGGTATCCGAGAGGACACTTGGCAAGGTCACCGATG	269
Db	37	GGAGGCTCAGACATCCACGCCCTTTGGTATCCGAGAGGACACTTGGCAAGGTCACCGATG	96
OY	270	GTCCGAGATCCACAACAAGACTGGCGGAGGAGGAGGAGAGACTTCTGTGTGCTTG	329
Db	97	GTCCGAGATCCACAACAAGACTGGCGGAGGAGGAGGAGAGACTTCTGTGTGCTTG	156
OY	330	GTTGGACAGTAAAGAGGCTCTTGGCCAGTCCAGGGTGGGGGGCGGCAAACTCCATTAAGAA	389
Db	157	GTTGGACAGTAAAGAGGCTCTTGGCCAGTCCAGGGTGGGGGGCGGCAAACTCCATTAAGAA	216
OY	390	CCAGAGGGTCTGGGGCCCCGGGCCACAAGATCAATTCGCCAGCTCCTCTGCTGTGGCCAGT	449
Db	217	CCAGAGGGTCTGGGGCCCCGGGCCACAAGATCAATTCGCCAGCTCCTCTGCTGTGGCCAGT	276
OY	450	GGGAGTGGCAAGAGGTGGGGCTTTGTGCCAGTAAAAACAAGGCTGAAATTTGCTTCGGGG	509
Db	277	GGGAGTGGCAAGAGGTGGGGCTTTGTGCCAGTAAAAACAAGGCTGAAATTTGCTTCGGGG	336
OY	510	CCATGTCCTCTGTCTAGGGCAGCAATTCACACTTCTTGTCTCTAGGACCCCAAAAGGC	569
Db	337	CCATGTCCTCTGTCTAGGGCAGCAATTCACACTTCTTGTCTCTAGGACCCCAAAAGGC	396
OY	570	TTTCATTGTATCTAATTTGAATTTTTCACATTAGCAATTTAAA--CTGAAATATGGGCGG	627
Db	397	TTTCATTGTATCTAATTTGAATTTTTCACATTAGCAATTTAAAATTTGAGAAATTTGGGCGG	456
OY	628	GCACGGTGGCTCACGCGCTGTATATCCACACTTTTGGAGGCGGAGCGGCTGATCA--CC	686
Db	457	GCACGGTGGCTCACGCGCTGTATATCCACACTTTTGGAGGCGGAGCGGCTGATCAACC	516
OY	687	TGAGATCAGG--AGTTCAAGACCAAG--CCTGGCCCAACATGCTGAACCTTGTCT--ACTRA	741
Db	517	TGAGATCAGGAAGTTCAAGACCAAGCGCTGGGCCCAATGCTGAAAACTTGTGCTTACTTAA	576
OY	742	AAATTCAAAAAATTAGCC	759
Db	577	AAATTCAAAAAATTAGCC	594

RESULT 6	AA664988/c	480 bp	mRNA	linear	EST 10-JUN-199
LOCUS					
DEFINITION	x800a06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone				
IMAGE	810034 5', mRNA sequence.				
ACCESSION	AA664988				
VERSION	AA664988.1	GI:2189872			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
	1 (bases 1 to 480)				
REFERENCE	Hillier,L., Allen,M., Bowles,J., Dubuque,T., Geisels,G., Jost,S.,				
AUTHORS	Kucaba,T., Lacey,M., Le,N., Lennon,G., Maira,M., Martin,J.,				
	Moore,B., Schellendberg,K., Steptoe,M., Tan,F., Theising,B.,				
	White,Y., Wylie,T., Waterson,K. and Wilson,K.				
TITLE	Washu-Merck EST Project 1997				


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Db      186  |||||GGCCACAGATCATCTGCGCCAGCTCTCTGCTGCGGCAAGTGGAGCGACGAGTGG 127
Oy      468  GCGTTTGCCAGTAAACACACAGGCTGGATTTGCTGCGGCCATGTCCTCTGCTAGG 527
Db      126  GCGTTTGCCAGTAAACACACAGGCTGGATTTG-CTGCGGCCCAATGCTCTGCTAGG 68
Oy      528  GCAGCAATTCCTCAACCTTCTGCTCTGACGAGCCCAAGAGCTTCATTGATCTATTGA 587
Db      67  GCAGCAATTCCTCAACCTTCTGCTCTGACGAGCCCAAGAGCTTCATTGATCTATTGA 8
Oy      588  TTTTAC 594
Db      7  TTTTAC 1

RESULT 8
AA399124/c 402 bp mRNA linear EST 16-MAY-1997
LOCUS z49a02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:725642 5', mRNA sequence.
ACCESSION AA399124
VERSION AA399124.1 GI:2052862
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 402)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kuuba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washu-Merck EST Project 1997
Unpublished (1997)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 279.
FEATURES
source
location/Qualifiers
1..402
/molecule="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5937549"
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/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/note="Organ: ovary; Vector: pRT3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGTTTATTTTATTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT3D vector
(Pharmacia). Library constructed by Bento Soares and
M.Facima Bernaldo."
ORIGIN
Query Match 40.7%; Score 369; DB 1; Length 402;
Best Local Similarity 99.3%; Pred. No.1,6e-50;
Matches 402; Conservative 0; Mismatches 0; Indels 3; Gaps 3;
190 TCTTGAGTCAAGGACGACGAGGACGCTCAACAGCTCCAGCCCTTTGTTACCGAGAGCA 249
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Db      402  TCTTGAGTCAAGGACGACGAGGACGCTCAACAGCTCCAGCCCTTTGTTACCGAGAGCA 343
Oy      250  CTTGGCAAGGTCACGCATGATGTCGAGTCCACACACAGACTGGCGCAGAGAGG 309
Db      342  CTTGGCAAGTTCACGCATGATGTCGAGTCCACACACAGACTGGCGCAGAGAGG 283
Oy      310  GGAAGTTCTGTTGCTTGGTGGAGAGTGAAGAGGCTTTGGCAGTCAAGGTTGGG 369
Db      282  GGAAGTTCTGTTGCTTGGTGGAGAGTGAAGAGGCTTTGGCAGTCAAGGTTGGG 223
Oy      370  GCGGCAATCTCCAAAGAACACAGAGGCTCGGGCCCGCCACAGAGTATCTGGCCAG 429
Db      222  GCGGCAATCTCCAAAGAACACAGAGGCTCGGGCCCGCCACAGAGTATCTGGCCAG 164
Oy      430  CTCCTGCTGCTGCGGACAGTGGAGTGGACAGAGTGGGCTTTGTCAGTAAACAC 489
Db      163  CTCCTGCTGCTGCGGACAGTGGAGTGGACAGAGTGGGCTTTGTCAGTAAACAC 104
Oy      490  AGGCTGATTTGCTGCGGACAGTGGTCCCTGCTAGGCGACAGCAATTCACCTCTTG 549
Db      103  AGGCTGATTTG-CTGCGGGCAGT-GTCCCTGCTAGGCGACAGCAATTCACCTCTTG 46
Oy      550  CTCACAGACCCCAAGAGCTTCATTGATCTATTGATTTTAC 594
Db      45  CTCACAGACCCCAAGAGCTTCATTGATCTATTGATTTTAC 1

RESULT 9
AA481356/c 360 bp mRNA linear EST 08-AUG-1997
LOCUS zv44d03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
DEFINITION IMAGE:756485 5', mRNA sequence.
ACCESSION AA481356
VERSION AA481356.1 GI:2210908
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 360)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kuuba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washu-Merck EST Project 1997
Unpublished (1997)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 219.
FEATURES
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location/Qualifiers
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/sex="Female"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares ovary tumor NbHOT"
/note="Organ: ovary; Vector: pRT3D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCGGTTTATTTTATTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pRT3D vector

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ORIGIN

(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo. "

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Query Match      37.9%; Score 344.2; DB 1; Length 360;
Best Local Similarity 98.9%; Pred. No. 1.8e-46;
Matches 357; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY 234 TGTTCACGAGAGACACTTGGCAAGTCCAGAGTCCGAGTCCACACAGACTGG 293
DB 360 TGTTCACGAGAGACACTTGGCAAGTCCAGAGTCCGAGTCCACACAGACTGG 301
QY 294 CGGCAAGGAGAGAGGAGGAGCACTTCTGTGTGCTTGTGGACAGTAAAGGGTCTTGGC 353
DB 300 CGGCAAGGAGAGAGGAGGAGCACTTCTGTGTGCTTGTGGACAGTAAAGGGTCTTGGC 241
QY 354 CAGTCCAGAGTGGGGGGGGCGGCAAACTCCATAAAGAACAGAGGGTCTGGGCCCGGAC 413
DB 240 CAGTCCAGAGTGGGGGGGGCGGCAAACTCCATAAAGAACAGAGGGTCTGGGCCCGGAC 182
QY 414 AGAGTCATCTGCCAGCTCTCTGTGCTGTGCGCAGTGGAGTGGACAGAGTGGGGCTTT 473
DB 181 AGAGTCATCTGCCAGCTCTCTGTGCTGTGCGCAGTGGAGTGGACAGAGTGGGGCTTT 122
QY 474 GTGCCAGTAAACCAAGGCTGATTTGCTGTGGGGCCATGGTCCCTGTCTTAGGGCAGCA 533
DB 121 GTGCCAGTAAACCAAGGCTGATTTGCTGTGGGGCCATGGTCCCTGTCTTAGGGCAGCA 62
QY 534 ATTCTCAACCTTCTGTCTCTCAGAGACCCCAAGAGCTTTCATGATCATGATTTTAA 593
DB 61 ATTCTCAACCTTCTGTCTCTCAGAGACCCCAAGAGCTTTCATGATCATGATTTTAA 2
QY 594 C 594
DB 1 C 1

```

RESULT 10
BM854082 547 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST0136380 S22SNUI6n1 Homo sapiens cDNA clone S22SNUI6n1-145-D09
DEFINITION 5', mRNA sequence.

ACCESSION BM854082
VERSION BM854082.1 GI:19210481
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 547)
Oh,K.J., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Kim,K.J., Cheong,J.B., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

TITLE Kim,Y.S.
JOURNAL 21C Frontier Korean EST Project 2001
COMMENT Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 145 row: D column: 09
High quality sequence stop: 547.

FEATURES

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ORIGIN

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Site 2: NotI; The S22SNUI6 library was contributed by the
Soares laboratory and it was constructed as described by
Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
Research 6(9): 791-806. RNA was prepared from harvested
cells of SNU-16 culture. SNU-16 cell was obtained from
Korean Cell Line Bank (KCLB). SNU-16 was established from
ascitic fluids of Korean patients by Park U.G. et al.
(1990), Cancer Res 50: 2773-2780."

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QY 1 GGACTGGAAGTCCCAAGAGCTGTGAGGCCCCCAAGAAAGTGTTCACACTTGGAC 60
DB 212 GAACTGGAAGTCCCAAGAGCTGTGAGGCCCCCAAGAAAGTGTTCACACTTGGAC 271
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DB 272 CCTAGAGGGTCTGGAATTTGTGTGTTAACAGATAAAGTGAAGGAGGAGACCCATAGGGGA 331
QY 121 ATGTACTCTCTGCTTCCCTTCCACTGCTGCTGTGTTCAGAGTGGCTGGTCCCTCTTGGC 180
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DB 452 GAGAGACACTTGGCAAGGTCAGGAGTGTCCGAGTCCACACACAGACTGGCGGACAG 511
QY 301 GCAAGAGGGGAGACAGTCTGTGTGCTTGTGTGGAC 336
DB 512 GCAAGAGGGGAGACAGTCTGTGTGCTTGTGTGGAC 547

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RESULT 11
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ACCESSION BF963567.1 GI:12380751
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 511)
Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Brito, M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongseneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PubMed 10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

AUTHORS
 Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R., Labkowski, J. and Stanton, L.W.
TITLE
 Transcriptional characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL
 Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT
 Contact: Brandenberger R
 Regenerative Medicine
 Genon Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@genon.com
 Insert Length: 308 Std Error: 0.00.

FEATURES
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 DB 241 AGTCCAGTCTCTCGGAGGCTGAGCGAGAAATGCTTGAACCCAGAGCGGACGTT 300
 QY 842 GCGGTGAG 849
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 DB 301 GCGGTGAG 308

RESULT 14
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 ACCESSION AL133867
 VERSION AL133867.1 GI:6602054
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 SOURCE Homo sapiens (human)
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REFERENCE
 1 (bases 1 to 363)
 Ansoorge, W., Winkner, U., Mewes, W., Wei, B. and Wiemann, S.
 EST (Ansoorge, W., Winkner, U., Mewes, H.W., Wei, B. and Wiemann, S.)
 JOURNAL Unpublished (1999)

COMMENT
 Contact: MIPS
 MIPS
 Ingolstaedter Landstr. 1, D-85764 Neuberg, Germany
 This is the 5' sequence of the clone insert
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;
 sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
 No si sequence available.
 This clone (DKFZP761H1914) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
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 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
 1 (bases 1 to 319)
 Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Brites, M.R., Nagel, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsumura, A., Bala, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.O., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 JOURNAL MEDLINE 20202663

PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br

This sequence was derived from the PAPSP/LICR Human Cancer Genome
 project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&t2=PM1-MT0198-
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 Seq primer: puc 18 forward
 High quality sequence start: 19
 High quality sequence stop: 319.
 Location/Qualifiers

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 from ORESTES PCR (U.S. Letters Patent application No.
 196,716 - Ludwig Institute for Cancer Research) profiles
 into the pUC 18 vector. Reverse transcription of tissue
 mRNA and cDNA amplification were performed under low
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ORIGIN

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 Best Local Similarity 92.8%; Pred. No. 1.5e-34;
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Db	259	AGGACCCCATAGGGGAATGCTA	CTGCTGCTTCCACCTGCTGCTTCA	CGGTGGC 200
QY	165	CTGTGCTCTCTTGGCCGAGAGATGTCCTGGGTCAAGGACGAGACGCTCA	CAGACT	224
Db	199	CTGTGCTCTCTTGGCCGAGAGATGTCCTGGGTCAAGGACGAGACGCTCA	CAGACT	140
QY	225	CCAGCCCTTTGTACCGAGAGACA	CTTGGCAAGTCCAGCATGTC	CGAGTCCAC 284
Db	139	CCAGCCCTTTGTACCGAGAGACA	CTTGGCAAGTCCAGCATGTC	CGAGTCCAC 80
QY	285	ACA--GACTGGCGGAGGCGAGAGGGGACATTTCTGTGTGCTTGGTTGA	CAGTAAG	342
Db	79	ACATGACTGGCGGAGGCGAGAGGGGACATTTCTGTGTGCTTGGTTGA	CAGTAAG	20
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Search completed: September 15, 2005, 18:10:57
 Job time : 3919 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2005, 15:49:33 ; Search time 4378 Seconds
(without alignments)
10038.575 Million cell updates/sec

Title: US-09-989-733-398

Perfect score: 907

Sequence: 1 ggaactctgaagtcacgaacg.....gtgagactccatctcacaca 907

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1_0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 1500 summaries

Database:

GenEmbl:*
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2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pac:*
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9: gb_pr:*
10: gb_ro:*
11: gb_str:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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23	214.4	23.6	93033	2	AP000644 Homo sapi
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25	214	23.6	194020	9	HUAC004125
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28	213.8	23.6	101768	9	AC006465 Homo sapi
29	213.8	23.6	165617	9	CNS0000K
30	213.8	23.6	207682	9	AC012564 Homo sapi
31	213.6	23.6	482	9	AY190784 Homo sapi
32	213.6	23.6	482	9	AY190786 Pan trogl
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40	213	23.5	41461	9	AC010646 Homo sapi
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47	212.6	23.4	171615	2	AC089988 Homo sapi
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49	212.6	23.4	231371	2	BX284617 Homo sapi
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57	212.4	23.4	180117	2	AC022526 Homo sapi
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60	212.2	23.4	134882	2	AC008622 Homo sapi
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90	211.2	23.3	1973	9	AK130331 Homo sapi
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92	211.2	23.3	138532	9	AC004812 Homo sapi

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108	210.6	23.2	177250	2	AP000778	AP000778 Homo sapi	c 181	209.2	23.1	183827	9	AC005899	AC005899 Homo sapi
109	210.4	23.2	85461	9	HS4151N12	AL109835 Human DNA	c 182	209.2	23.1	184121	9	AC023119	AC023119 Homo sapi
110	210.4	23.2	91722	9	AC090114	AC090114 Homo sapi	c 183	209.2	23.1	184841	2	AC129486	AC129486 Homo sapi
111	210.4	23.2	162817	2	AC150233	AL442663 Human chr	c 184	209.2	23.1	185049	9	AL365495	AL365495 Homo sapi
112	210.4	23.2	165423	9	CNS07ECV	AL442663 Human chr	c 185	209.2	23.1	186325	2	AC074244	AC074244 Homo sapi
113	210.4	23.2	168860	9	AL160175	AL160175 Human DNA	c 186	209.2	23.1	199275	9	AC011401	AC011401 Homo sapi
114	210.4	23.2	190107	9	ALC100832	AC100832 Homo sapi	c 187	209.2	23.1	205342	9	AC068282	AC068282 Homo sapi
115	210.4	23.2	306749	2	AL1590310	AL1590310 Homo sapi	c 188	209.2	23.1	207822	2	AC109321	AC109321 Homo sapi
116	210.2	23.2	59634	9	AC062028	AC062028 Homo sapi	c 189	209.2	23.1	220184	9	AC008026	AC008026 Homo sapi
117	210.2	23.2	104395	9	AC092469	AC092469 Homo sapi	c 190	209.2	23.0	62550	2	AC090460	AC090460 Homo sapi
118	210.2	23.2	160001	2	AC125515	AC125515 Pan trogl	c 191	209.2	23.0	73322	2	AC069380	AC069380 Homo sapi
119	210.2	23.2	301	6	AX741027	AX741027 Sequence	c 192	209.2	23.0	84323	9	HS138B7	HS138B7 Homo sapi
120	210.2	23.2	152036	2	AL161776	AL161776 Homo sapi	c 193	209.2	23.0	125000	9	AB017602	AB017602 Homo sapi
121	210.2	23.2	179308	9	AC114402	AC114402 Homo sapi	c 194	209.2	23.0	125376	9	AP001627	AP001627 Homo sapi
122	210.2	23.2	190185	9	AC026464	AC026464 Homo sapi	c 195	209.2	23.0	130328	2	AC079622	AC079622 Homo sapi
123	210.2	23.2	196220	9	AC026474	AC026474 Homo sapi	c 196	209.2	23.0	133587	2	AL445648	AL445648 Homo sapi
124	210.2	23.2	226170	9	AC008761	AC008761 Homo sapi	c 197	209.2	23.0	145762	9	AP001626	AP001626 Homo sapi
125	209.8	23.1	51474	6	BD093705	BD093705 Human 1p3	c 198	209.8	23.0	161506	9	AL450105	AL450105 Homo sapi
126	209.8	23.1	68622	2	AP003163	AP003163 Homo sapi	c 199	209.8	23.0	161990	2	AL357313	AL357313 Homo sapi
127	209.8	23.1	94422	9	HS575L21	AL096841 Human DNA	c 200	209.8	23.0	163942	9	AC016245	AC016245 Homo sapi
128	209.8	23.1	121628	9	AC117517	AC117517 Homo sapi	c 201	209.8	23.0	167996	9	AC021753	AC021753 Homo sapi
129	209.8	23.1	122888	9	HS333H23	AL022326 Human DNA	c 202	209.8	23.0	180623	2	AC092341	AC092341 Homo sapi
130	209.8	23.1	131185	9	AC096946	AC096946 Homo sapi	c 203	209.8	23.0	181161	2	AC092347	AC092347 Homo sapi
131	209.8	23.1	144046	2	AC068334	AC068334 Homo sapi	c 204	209.8	23.0	182598	2	AC064818	AC064818 Homo sapi
132	209.8	23.1	144818	9	AL139343	AL139343 Human DNA	c 205	209.8	23.0	186197	2	AL627384	AL627384 Homo sapi
133	209.8	23.1	146167	9	AC087588	AC087588 Homo sapi	c 206	209.8	23.0	189356	9	AC005746	AC005746 Homo sapi
134	209.8	23.1	152511	2	AC019269	AC019269 Homo sapi	c 207	209.8	23.0	199669	9	AC026469	AC026469 Homo sapi
135	209.8	23.1	163360	2	AL021598	AL021598 Homo sapi	c 208	209.8	23.0	229267	2	AC145242	AC145242 Homo sapi
136	209.8	23.1	166016	9	AL591378	AL591378 Human DNA	c 209	209.8	23.0	340000	9	AP001747	AP001747 Homo sapi
137	209.8	23.1	166128	9	AP003774	AP003774 Homo sapi	c 210	209.8	23.0	43712	9	HS984G1	HS984G1 Homo sapi
138	209.8	23.1	166356	9	AP001453	AP001453 Homo sapi	c 211	209.8	23.0	102714	9	AP000692	AP000692 Homo sapi
139	209.8	23.1	174649	2	AC068210	AC068210 Homo sapi	c 212	209.8	23.0	125508	9	AC006345	AC006345 Homo sapi
140	209.8	23.1	206395	9	AC008759	AC008759 Homo sapi	c 213	209.8	23.0	127078	9	AP000708	AP000708 Homo sapi
141	209.8	23.1	213447	2	AC083833	AC083833 Homo sapi	c 214	209.8	23.0	132875	9	AC112907	AC112907 Homo sapi
142	209.6	23.1	39910	9	AP001039	AP001039 Homo sapi	c 215	209.8	23.0	134620	9	BX119917	BX119917 Homo sapi
143	209.6	23.1	102313	9	AL1603749	AL1603749 Human DNA	c 216	209.8	23.0	153392	9	AL133548	AL133548 Homo sapi
144	209.6	23.1	105079	9	AL513008	AL513008 Human DNA	c 217	209.8	23.0	156655	9	HSN14	HSN14 Homo sapi
145	209.6	23.1	132068	9	AC006965	AC006965 Homo sapi	c 218	209.8	23.0	165332	2	AC011680	AC011680 Homo sapi
146	209.6	23.1	147054	2	AL356582	AL356582 Homo sapi	c 219	209.8	23.0	171976	9	AP003069	AP003069 Homo sapi
147	209.6	23.1	166258	2	AL451066	AL451066 Homo sapi	c 220	209.8	23.0	172600	9	AL359644	AL359644 Homo sapi
148	209.6	23.1	167548	9	AL1391809	AL1391809 Human DNA	c 221	209.8	23.0	173472	2	AC098807	AC098807 Homo sapi
149	209.6	23.1	184591	9	AL355443	AL355443 Human DNA	c 222	209.8	23.0	173472	2	AC144466	AC144466 Homo sapi
150	209.6	23.1	206246	2	AL606485	AL606485 Homo sapi	c 223	209.8	23.0	193168	2	AC011969	AC011969 Homo sapi
151	209.6	23.1	340000	9	AP001732	AP001732 Homo sapi	c 224	209.8	23.0	195323	2	AC026612	AC026612 Homo sapi
152	209.4	23.1	1946	12	SYNAD5SRC	M34061 Synthetic h	c 225	209.8	23.0	340000	2	AP001725	AP001725 Homo sapi
153	209.4	23.1	2725	12	HSAD5A	X71401 H.sapiens a	c 226	209.8	23.0	84278	2	AC024907_3	Continuation (4 of
154	209.4	23.1	108508	9	AC133539	AC133539 Homo sapi	c 227	209.8	23.0	111104	9	AC117389	AC117389 Homo sapi
155	209.4	23.1	147878	9	AC024600	AC024600 Homo sapi	c 228	209.8	23.0	120725	9	AC084123	AC084123 Homo sapi
156	209.4	23.1	174968	2	AL928903	AL928903 Homo sapi	c 229	209.8	23.0	120739	2	AL807782	AL807782 Homo sapi
157	209.4	23.1	177332	9	AL139385	AL139385 Human DNA	c 230	209.8	23.0	131429	9	AC124159	AC124159 Homo sapi
158	209.4	23.1	192462	9	CNS01RHC	AL161665 Human chr	c 231	209.8	23.0	135770	9	CR631130	CR631130 Homo sapi
159	209.4	23.1	192801	2	AC134308	AC134308 Homo sapi	c 232	209.8	23.0	143409	2	AP001787	AP001787 Homo sapi
160	209.4	23.1	193047	2	AC120780	AC120780 Pan trogl	c 233	209.8	23.0	148654	9	AL683813	AL683813 Homo sapi
161	209.4	23.1	194191	2	AC097332	AC097332 Pan trogl	c 234	209.8	23.0	149172	9	AP315312	AP315312 Homo sapi
162	209.4	23.1	201155	9	AC009086	AC009086 Homo sapi	c 235	209.8	23.0	149409	9	AC004081	AC004081 Homo sapi
163	209.4	23.1	216497	9	HS037C10	AL049366 Human DNA	c 236	209.8	23.0	150800	9	AC027176	AC027176 Homo sapi
164	209.4	23.1	252512	2	AC097326	AC097326 Pan trogl	c 237	209.8	23.0	165662	9	AC092070	AC092070 Homo sapi
165	209.2	23.1	50000	6	AX393458	AX393458 Sequence	c 238	209.6	23.0	169725	9	AP000879	AP000879 Homo sapi

239	208.6	23.0	170908	9	HSBA28009	AL121582	Human	DNA	C	312	208	22.9	275197	9	AC004166	AC004166	Human	gadi	C	312	208	22.9	275197	9	AC004166	AC004166	Human	gadi	
240	208.6	23.0	171813	2	AC022722	AC022722	Human	gadi	C	313	207.8	22.9	72240	9	CR759873	CR759873	Human	DNA	C	313	207.8	22.9	72240	9	CR759873	CR759873	Human	DNA	
241	208.6	23.0	173645	2	AC010770	AC010770	Human	gadi	C	314	207.8	22.9	78229	9	AC117447	AC117447	Human	gadi	C	314	207.8	22.9	78229	9	AC117447	AC117447	Human	gadi	
242	208.6	23.0	180227	9	AC091100	AC091100	Human	gadi	C	315	207.8	22.9	80743	9	AL6073422	AL6073422	Human	gadi	C	315	207.8	22.9	80743	9	AL6073422	AL6073422	Human	gadi	
243	208.6	23.0	181833	9	CNS05TEN	AL359235	Human	chr	C	316	207.8	22.9	133290	9	AL627402	AL627402	Human	DNA	C	316	207.8	22.9	133290	9	AL627402	AL627402	Human	DNA	
244	208.6	23.0	181833	9	AL606804	AL606804	Human	DNA	C	317	207.8	22.9	133912	9	AL358075	AL358075	Human	DNA	C	317	207.8	22.9	133912	9	AL358075	AL358075	Human	DNA	
245	208.6	23.0	187314	2	AC026590	AC026590	Human	gadi	C	318	207.8	22.9	139267	9	AC006435	AC006435	Human	gadi	C	318	207.8	22.9	139267	9	AC006435	AC006435	Human	gadi	
246	208.6	23.0	187936	9	AC080003	AC080003	Human	gadi	C	319	207.8	22.9	142085	9	AL359707	AL359707	Human	DNA	C	319	207.8	22.9	142085	9	AL359707	AL359707	Human	DNA	
247	208.6	23.0	188829	2	AC013281	AC013281	Human	gadi	C	320	207.8	22.9	148509	9	AC068014	AC068014	Human	gadi	C	320	207.8	22.9	148509	9	AC068014	AC068014	Human	gadi	
248	208.6	23.0	190842	2	AC006235	AC006235	Human	gadi	C	321	207.8	22.9	152167	2	AP000486	AP000486	Human	gadi	C	321	207.8	22.9	152167	2	AP000486	AP000486	Human	gadi	
249	208.6	23.0	193314	2	AC087478	AC087478	Human	gadi	C	322	207.8	22.9	152442	2	AC024960	AC024960	Human	gadi	C	322	207.8	22.9	152442	2	AC024960	AC024960	Human	gadi	
250	208.6	23.0	193314	2	AC087478	AC087478	Human	gadi	C	323	207.8	22.9	153241	2	AC027817	AC027817	Human	gadi	C	323	207.8	22.9	153241	2	AC027817	AC027817	Human	gadi	
251	208.6	23.0	195068	9	AC012314	AC012314	Human	gadi	C	324	207.8	22.9	154565	2	AL138720	AL138720	Human	DNA	C	324	207.8	22.9	154565	2	AL138720	AL138720	Human	DNA	
252	208.6	23.0	198017	9	AC012314	AC012314	Human	gadi	C	325	207.8	22.9	156615	9	AC008511	AC008511	Human	gadi	C	325	207.8	22.9	156615	9	AC008511	AC008511	Human	gadi	
253	208.6	23.0	205307	2	AC009968	AC009968	Human	gadi	C	326	207.8	22.9	160770	2	AC084778	AC084778	Human	gadi	C	326	207.8	22.9	160770	2	AC084778	AC084778	Human	gadi	
254	208.6	23.0	233231	2	AC022220	AC022220	Human	gadi	C	327	207.8	22.9	161740	2	AC084623	AC084623	Human	gadi	C	327	207.8	22.9	161740	2	AC084623	AC084623	Human	gadi	
255	208.4	23.0	43715	9	AC093298	AC093298	Human	gadi	C	328	207.8	22.9	163969	2	BSX284623	BSX284623	Human	gadi	C	328	207.8	22.9	163969	2	BSX284623	BSX284623	Human	gadi	
256	208.4	23.0	74932	9	AC008762	AC008762	Human	gadi	C	329	207.8	22.9	166181	9	HS375E16	HS375E16	Human	gadi	C	329	207.8	22.9	166181	9	HS375E16	HS375E16	Human	gadi	
257	208.4	23.0	115345	9	AC008147	AC008147	Human	gadi	C	330	207.8	22.9	171411	2	AC087609	AC087609	Human	gadi	C	330	207.8	22.9	171411	2	AC087609	AC087609	Human	gadi	
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259	208.4	23.0	131967	9	AL161622	AL161622	Human	DNA	C	332	207.8	22.9	181265	2	AC0019356	AC0019356	Human	gadi	C	332	207.8	22.9	181265	2	AC0019356	AC0019356	Human	gadi	
260	208.4	23.0	132805	9	HS339A18	Z97054	Human	DNA	C	333	207.8	22.9	184111	9	AC008821	AC008821	Human	gadi	C	333	207.8	22.9	184111	9	AC008821	AC008821	Human	gadi	
261	208.4	23.0	1484289	2	AL109851	Human	DNA	B	C	334	207.8	22.9	190765	9	AL359763	AL359763	Human	DNA	C	334	207.8	22.9	190765	9	AL359763	AL359763	Human	DNA	
262	208.4	23.0	179627	2	AC113426	AC113426	Human	gadi	C	335	207.8	22.9	210799	2	AC013721	AC013721	Human	gadi	C	335	207.8	22.9	210799	2	AC013721	AC013721	Human	gadi	
263	208.4	23.0	179627	2	AC113426	AC113426	Human	gadi	C	336	207.8	22.9	254633	2	CR762389	CR762389	Danio rerio	gadi	C	336	207.8	22.9	254633	2	CR762389	CR762389	Danio rerio	gadi	
264	208.4	23.0	207751	2	AC124859	AC124859	Human	gadi	C	337	207.6	22.9	31766	6	AX354725	AX354725	Sequence		C	337	207.6	22.9	31766	6	AX354725	AX354725	Sequence		
265	208.2	23.0	207751	2	AC008902	AC008902	Human	gadi	C	338	207.6	22.9	34366	9	AC090632	AC090632	Human	gadi	C	338	207.6	22.9	34366	9	AC090632	AC090632	Human	gadi	
266	208.2	23.0	119072	9	AL136531	AL136531	Human	DNA	C	339	207.6	22.9	38852	2	AC006261	AC006261	Human	gadi	C	339	207.6	22.9	38852	2	AC006261	AC006261	Human	gadi	
267	208.2	23.0	126231	9	AC0004139	AC0004139	Human	DNA	C	340	207.6	22.9	62319	2	AC132200	AC132200	Human	gadi	C	340	207.6	22.9	62319	2	AC132200	AC132200	Human	gadi	
268	208.2	23.0	131990	9	AC008925	AC008925	Human	gadi	C	341	207.6	22.9	113456	9	HS4498B10	HS4498B10	Human	DNA	C	341	207.6	22.9	113456	9	HS4498B10	HS4498B10	Human	DNA	
269	208.2	23.0	133867	9	AL353648	AL353648	Human	DNA	C	342	207.6	22.9	129430	9	AL358113	AL358113	Human	DNA	C	342	207.6	22.9	129430	9	AL358113	AL358113	Human	DNA	
270	208.2	23.0	141923	2	AC109997	AC109997	Human	DNA	C	343	207.6	22.9	129719	9	AC020922	AC020922	Human	gadi	C	343	207.6	22.9	129719	9	AC020922	AC020922	Human	gadi	
271	208.2	23.0	145388	9	HS390013	Z84469	Human	DNA	B	C	344	207.6	22.9	134793	2	AC073398	AC073398	Human	gadi	C	344	207.6	22.9	134793	2	AC073398	AC073398	Human	gadi
272	208.2	23.0	147364	9	AL1732602	AL1732602	Human	DNA	C	345	207.6	22.9	137922	2	AC136365	AC136365	Human	gadi	C	345	207.6	22.9	137922	2	AC136365	AC136365	Human	gadi	
273	208.2	23.0	153438	2	AC069480	AC069480	Human	gadi	C	346	207.6	22.9	143757	9	AP005902	AP005902	Human	gadi	C	346	207.6	22.9	143757	9	AP005902	AP005902	Human	gadi	
274	208.2	23.0	163149	2	CNS01DSZ	AL122057	Human	chr	C	347	207.6	22.9	149577	9	AC0005478	AC0005478	Human	gadi	C	347	207.6	22.9	149577	9	AC0005478	AC0005478	Human	gadi	
275	208.2	23.0	1631705	2	AC023774	AC023774	Human	gadi	C	348	207.6	22.9	150140	2	AC009157	AC009157	Human	gadi	C	348	207.6	22.9	150140	2	AC009157	AC009157	Human	gadi	
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277	208.2	23.0	163876	2	AC016402	AC016402	Human	gadi	C	350	207.6	22.9	157850	9	AL3625325	AL3625325	Human	gadi	C	350	207.6	22.9	157850	9	AL3625325	AL3625325	Human	gadi	
278	208.2	23.0	169326	9	AC009783	AC009783	Human	gadi	C	351	207.6	22.9	163567	2	AC022210	AC022210	Human	gadi	C	351	207.6	22.9	163567	2	AC022210	AC022210	Human	gadi	
279	208.2	23.0	169326	9	AC009783	AC009783	Human	gadi	C	352	207.6	22.9	164607	9	AC022210	AC022210	Human	gadi	C	352	207.6	22.9	164607	9	AC022210	AC022210	Human	gadi	
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281	208.2	23.0	174591	9	AC109335	AC109335	Human	gadi	C	354	207.6	22.9	165761	2	AC145750	AC145750	Human	gadi	C	354	207.6	22.9	165761	2	AC145750	AC145750	Human	gadi	
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284	208.2	23.0	195523	9	AC018642	AC018642	Human	gadi	C	357	207.6	22.9	171007	2	AC131095	AC131095	Human	gadi	C	357	207.6	22.9	171007	2	AC131095	AC131095	Human	gadi	
285	208.2	23.0	213745	9	AC009712	AC009712	Human	gadi	C	358	207.6	22.9	173627	9	AC099511	AC099511	Human	gadi	C	358	207.6	22.9	173627	9	AC099511	AC099511	Human	gadi	
286	208.2	23.0	213745	9	AC009712	AC009712	Human	gadi	C	359	207.6	22.9	176584	2	AC018494	AC018494	Human	gadi	C	359	207.6	22.9	176584	2	AC018494	AC018494	Human	gadi	
287	208.2	23.0	227137	9	AC0098481	AC0098481	Human																						

385	207.4	22.9	169554	2	AC021379	Homo sapi	458	207	22.8	217615	2	AC083976	Homo sapi
386	207.4	22.9	174535	2	AC106872	Homo sapi	459	207	22.8	227912	2	AC138930	Homo sapi
387	207.4	22.9	182428	2	AC036167	Homo sapi	460	207	22.8	241781	2	AC145097	Homo sapi
388	207.4	22.9	183976	2	AC100821	Homo sapi	461	207	22.8	250483	2	AC145096	Homo sapi
389	207.4	22.9	185571	9	AC133781	Homo sapi	462	206.8	22.8	69201	9	AC004109	Homo sapi
390	207.4	22.9	185602	9	AL139081	Human DNA	463	206.8	22.8	77425	9	AF068862	Homo sapi
391	207.4	22.9	188296	2	AC022324	Homo sapi	464	206.8	22.8	88395	9	AC004612	Homo sapi
392	207.4	22.9	188470	2	AC093005	Homo sapi	465	206.8	22.8	89352	9	AC006030	Homo sapi
393	207.4	22.9	191154	2	AC132150	Homo sapi	466	206.8	22.8	99108	9	AC008665	Homo sapi
394	207.4	22.9	193894	9	AC114730	Homo sapi	467	206.8	22.8	104148	9	AC006146	Homo sapi
395	207.4	22.9	196292	9	CNS00008	Homo sapi	468	206.8	22.8	116004	9	AF258545	Homo sapi
396	207.4	22.9	200711	2	AC133960	Homo sapi	469	206.8	22.8	121717	9	AL144548	Homo sapi
397	207.4	22.9	206587	9	AL138898	Human DNA	470	206.8	22.8	136882	9	AL1731574	Human DNA
398	207.4	22.9	207983	9	AC009960	Homo sapi	471	206.8	22.8	149790	9	AC022106	Homo sapi
399	207.4	22.9	219821	9	AC008738	Homo sapi	472	206.8	22.8	154577	2	AL357046	Homo sapi
400	207.2	22.8	47167	9	HS757P12	Homo sapi	473	206.8	22.8	161164	2	AC022278	Homo sapi
401	207.2	22.8	57084	2	AC129892	Homo sapi	474	206.8	22.8	162728	9	AP002906	Homo sapi
402	207.2	22.8	77880	9	AC114766	Homo sapi	475	206.8	22.8	164906	9	AC096637	Homo sapi
403	207.2	22.8	93847	9	AL157373	Homo sapi	476	206.8	22.8	168640	9	AC123779	Homo sapi
404	207.2	22.8	100719	9	BX255925	Human DNA	477	206.8	22.8	172614	9	AL929302	Homo sapi
405	207.2	22.8	121909	9	HS7492P14	Human DNA	478	206.8	22.8	173403	9	BS000114	Homo sapi
406	207.2	22.8	130526	2	AP000715	Homo sapi	479	206.8	22.8	174521	2	AC127468	Homo sapi
407	207.2	22.8	138846	2	AC068478	Homo sapi	480	206.8	22.8	175802	9	AC040174	Homo sapi
408	207.2	22.8	147534	9	AC068620	Homo sapi	481	206.8	22.8	176629	9	AC008641	Homo sapi
409	207.2	22.8	151889	9	AC084250	Homo sapi	482	206.8	22.8	177257	2	AL807789	Homo sapi
410	207.2	22.8	154639	2	AC090175	Homo sapi	483	206.8	22.8	184886	9	AC016650	Homo sapi
411	207.2	22.8	167102	9	AC084017	Homo sapi	484	206.8	22.8	185257	9	AL355305	Homo sapi
412	207.2	22.8	170722	9	AC087847	Homo sapi	485	206.8	22.8	193132	2	AC025743	Homo sapi
413	207.2	22.8	170877	2	AC025610	Homo sapi	486	206.8	22.8	196772	2	AC087392	Homo sapi
414	207.2	22.8	171035	9	AC016178	Homo sapi	487	206.8	22.8	199208	2	AC019236	Homo sapi
415	207.2	22.8	172403	2	AC017061	Homo sapi	488	206.8	22.8	205819	2	AC016805	Homo sapi
416	207.2	22.8	178917	9	AC021205	Homo sapi	489	206.8	22.8	208953	9	CNS01RH3	Homo sapi
417	207.2	22.8	183436	9	AC012489	Homo sapi	490	206.8	22.8	331864	9	AF049895	Homo sapi
418	207.2	22.8	193981	2	AC148832	Homo sapi	491	206.6	22.8	433919	9	AL446023	Homo sapi
419	207.2	22.8	202856	2	AC027374	Homo sapi	492	206.6	22.8	57494	9	BS000189	Homo sapi
420	207.2	22.8	210133	9	AC013564	Homo sapi	493	206.6	22.8	70148	9	AL357061	Homo sapi
421	207	22.8	2466	9	D89927	Human Na+/p	494	206.6	22.8	76792	9	AC023161	Homo sapi
422	207	22.8	38906	9	BX842243	Homo sapi	495	206.6	22.8	83731	2	AC079747	Homo sapi
423	207	22.8	39852	9	AC006128	Homo sapi	496	206.6	22.8	96608	9	HS308113	Homo sapi
424	207	22.8	41630	9	AC005785	Homo sapi	497	206.6	22.8	101861	2	AL359086	Homo sapi
425	207	22.8	46775	9	HS0738A13	Homo sapi	498	206.6	22.8	107438	9	AC005281	Homo sapi
426	207	22.8	65128	9	AC073188	Homo sapi	499	206.6	22.8	113109	9	HS475N16	Homo sapi
427	207	22.8	76354	9	AC048340	Homo sapi	500	206.6	22.8	116879	9	AC106854	Homo sapi
428	207	22.8	78167	9	AC092028	Homo sapi	501	206.6	22.8	120491	9	AC008859	Homo sapi
429	207	22.8	85787	9	AC073069	Homo sapi	502	206.6	22.8	127883	9	AL136141	Homo sapi
430	207	22.8	87386	9	AC133750	Homo sapi	503	206.6	22.8	129577	9	AC004659	Homo sapi
431	207	22.8	87758	9	AC068768	Homo sapi	504	206.6	22.8	141000	9	AC121756	Homo sapi
432	207	22.8	110000	2	AC140129 ⁻²	Continuation (3 of	505	206.6	22.8	143060	9	AL929472	Homo sapi
433	207	22.8	111312	9	AC011248	Homo sapi	506	206.6	22.8	147545	9	AC126614	Homo sapi
434	207	22.8	118131	2	AC055713	Homo sapi	507	206.6	22.8	148271	9	AL392046	Homo sapi
435	207	22.8	121353	2	AC023386	Homo sapi	508	206.6	22.8	154754	9	AC064836	Homo sapi
436	207	22.8	123529	9	AF179296	Homo sapi	509	206.6	22.8	158078	9	AC005094	Homo sapi
437	207	22.8	127867	9	HS694B14	Homo sapi	510	206.6	22.8	160723	9	AC010722	Homo sapi
438	207	22.8	132323	9	AC116615	Homo sapi	511	206.6	22.8	160981	9	AC103986	Homo sapi
439	207	22.8	139384	2	AC006455	Homo sapi	512	206.6	22.8	161421	2	AC026649	Homo sapi
440	207	22.8	149058	2	AC023065	Homo sapi	513	206.6	22.8	163972	9	AC103987	Homo sapi
441	207	22.8	152878	2	AC079190	Homo sapi	514	206.6	22.8	167998	9	AL353662	Homo sapi
442	207	22.8	171897	9	AC145098	Homo sapi	515	206.6	22.8	169736	2	AC019305	Homo sapi
443	207	22.8	173391	9	AC090063	Homo sapi	516	206.6	22.8	171990	9	AL137071	Homo sapi
444	207	22.8	174530	9	AL158835	Human DNA	517	206.6	22.8	172868	9	AC009117	Homo sapi
445	207	22.8	179759	2	AC132868	Homo sapi	518	206.6	22.8	173766	9	AC009117	Homo sapi
446	207	22.8	181864	2	AL353743	Homo sapi	519	206.6	22.8	175827	9	AL358472	Homo sapi
447	207	22.8	191280	2	AC087389	Homo sapi	520	206.6	22.8	177444	9	AC011468	Homo sapi
448	207	22.8	193519	2	AC023123	Homo sapi	521	206.6	22.8	178384	2	AL591026	Homo sapi
449	207	22.8	201886	2	AC140511	Homo sapi	522	206.6	22.8	180166	2	AC011898	Homo sapi
450	207	22.8	209859	2	AC084083	Homo sapi	523	206.6	22.8	183048	2	AC011656	Homo sapi
451	207	22.8	209870	2	AC104431	Homo sapi	524	206.6	22.8	185688	2	AC018805	Homo sapi
452	207	22.8	211810	2	AC026112	Homo sapi	525	206.6	22.8	187174	9	AC006241	Homo sapi
453	207	22.8	213861	9	AL135793	Homo sapi	526	206.6	22.8	191960	9	AC024475	Homo sapi
454	207	22.8	215808	9	AC140179	Homo sapi	527	206.6	22.8	196203	9	AL355355	Homo sapi
455	207	22.8	215936	9	CNS0507CA	Human chr	528	206.6	22.8	200464	2	AC148619	Homo sapi
456	207	22.8	216749	9	AC104319	Homo sapi	529	206.6	22.8	204793	2	AC026333	Homo sapi
457	207	22.8	216789	9	AC006534	Homo sapi	530	206.6	22.8	255952	2	AL513473	Homo sapi

531	206.4	22.8	3621	9	AY204748	604	206.2	22.7	187908	9	HS495010	AL031121	Human DNA
532	206.4	22.8	28420	9	AL162391	605	206.2	22.7	188666	9	AC018921	AC018921	Homo sapi
533	206.4	22.8	35666	9	BX119906	606	206.2	22.7	192618	9	AC092811	AC092811	Homo sapi
534	206.4	22.8	59356	9	AC115109	607	206.2	22.7	200000	9	AP000512	AP000512	Homo sapi
535	206.4	22.8	78415	9	BS000161	608	206.2	22.7	200430	9	AC011500	AC011500	Homo sapi
536	206.4	22.8	96594	6	AX6595647	609	206.2	22.7	201197	2	HS424J12	Z82207	Homo sapi
537	206.4	22.8	99592	9	AP263284	610	206.2	22.7	217035	9	AC099669	AC099669	Homo sapi
538	206.4	22.8	104658	9	AP006284	611	206.2	22.7	220007	2	AC148935	AC148935	Homo sapi
539	206.4	22.8	114517	9	AL158152	612	206.2	22.7	339168	2	AC078987	AC078987	Homo sapi
540	206.4	22.8	119951	2	AC0525267	613	206	22.7	50564	9	AY338490	AY338490	Homo sapi
541	206.4	22.8	120044	9	AL590116	614	206	22.7	51041	2	AP228703	AP228703	Homo sapi
542	206.4	22.8	145133	2	AC0138922	615	206	22.7	52459	9	HSJ735G18	AL118497	Human DNA
543	206.4	22.8	151498	9	AC0271139	616	206	22.7	55256	9	HS4329J7	AL1583856	Human DNA
544	206.4	22.8	154813	9	AC131934	617	206	22.7	73029	9	HSB41D10	Z97985	Human DNA
545	206.4	22.8	155539	9	AL138721	618	206	22.7	79555	9	HS431D10	AL664028	Human DNA
546	206.4	22.8	157242	2	AC083821	619	206	22.7	82517	9	AL664028	AL356748	Human DNA
547	206.4	22.8	159593	2	AC007924	620	206	22.7	97559	9	AL356748	AC005006	Homo sapi
548	206.4	22.8	160573	9	AC119676	621	206	22.7	1011720	9	AC005006	AC103959	Homo sapi
549	206.4	22.8	170862	2	AC087784	622	206	22.7	103584	9	CR752982	CR752982	Homo sapi
550	206.4	22.8	171818	9	AC063962	623	206	22.7	109576	2	AC114302	AC114302	Homo sapi
551	206.4	22.8	172963	9	AC134866	624	206	22.7	145327	9	AC144499	AC144499	Homo sapi
552	206.4	22.8	173099	9	AC092487	625	206	22.7	149714	2	AC073199	AC055711	Homo sapi
553	206.4	22.8	183301	2	AC092487	626	206	22.7	151933	2	AC055711	AL133336	Homo sapi
554	206.4	22.8	187294	9	AC084082	627	206	22.7	154850	2	AC055711	AL133336	Homo sapi
555	206.4	22.8	188639	9	AC011236	628	206	22.7	155559	2	HSN14	AP002442	Homo sapi
556	206.4	22.8	194746	2	AC145544	629	206	22.7	156655	2	AP002442	AP002442	Homo sapi
557	206.4	22.8	210636	9	AC006443	630	206	22.7	156620	2	AC009314	AC009314	Homo sapi
558	206.4	22.8	224187	9	AL7732374	631	206	22.7	161788	9	AC021755	AC021755	Homo sapi
559	206.4	22.8	241304	9	AL954220	632	206	22.7	161794	9	AC020687	AC020687	Homo sapi
560	206.4	22.8	250529	9	HUAE00658	633	206	22.7	169571	9	AC012146	AC012146	Homo sapi
561	206.2	22.7	4936	9	AF134406	634	206	22.7	171309	9	AC025168	AC025168	Homo sapi
562	206.2	22.7	21118	9	AF190749	635	206	22.7	173336	9	AC025168	AC025168	Homo sapi
563	206.2	22.7	22038	9	HSFPMG2	636	206	22.7	176277	2	AC139815	AC139815	Homo sapi
564	206.2	22.7	23332	9	AL591166	637	206	22.7	181916	2	AC117181	AC117181	Homo sapi
565	206.2	22.7	39198	6	AX078379	638	206	22.7	182892	9	AC034244	AC034244	Homo sapi
566	206.2	22.7	46610	9	HSU34879	639	206	22.7	185571	9	AC133781	AC133781	Homo sapi
567	206.2	22.7	56270	9	AC117435	640	206	22.7	185571	9	AC144518	AC144518	Homo sapi
568	206.2	22.7	71418	9	AL7732442	641	206	22.7	191414	2	AC009506	AC009506	Homo sapi
569	206.2	22.7	71503	9	AF219991	642	206	22.7	191764	9	AC140510	AC140510	Homo sapi
570	206.2	22.7	75074	9	CR788240	643	206	22.7	193879	2	AC114730	AC114730	Homo sapi
571	206.2	22.7	77908	9	AC008609	644	206	22.7	194516	9	AC024681	AC024681	Homo sapi
572	206.2	22.7	82636	9	AC086728	645	206	22.7	194516	9	AF215848	AF215848	Homo sapi
573	206.2	22.7	86937	2	AC108364	646	206	22.7	199451	2	AC087624	AC087624	Homo sapi
574	206.2	22.7	104755	9	BX908728	647	206	22.7	206596	2	AC087624	AC087624	Homo sapi
575	206.2	22.7	105104	9	HSJ47617	648	206	22.7	244847	2	AP002357	AP002357	Homo sapi
576	206.2	22.7	110000	2	AL831785_1	649	205.8	22.7	6905	9	HSFPMG4	UI8270	Human thymo
577	206.2	22.7	110000	2	BX294172_0	650	205.8	22.7	35886	9	AC004035	AC004035	Homo sapi
578	206.2	22.7	121212	9	HS135L22	651	205.8	22.7	36428	9	AC005362	AC005362	Homo sapi
579	206.2	22.7	123554	9	AB023049	652	205.8	22.7	44375	9	AC148448	AC148448	Homo sapi
580	206.2	22.7	129252	9	HSU91327	653	205.8	22.7	55588	9	AC073841	AC073841	Homo sapi
581	206.2	22.7	129747	9	HS465N24	654	205.8	22.7	59554	6	AX695587	AX695587	Sequence
582	206.2	22.7	130755	9	AL845353	655	205.8	22.7	74432	9	HS465G10B	Z94801	Human DNA
583	206.2	22.7	132066	9	AL953882	656	205.8	22.7	84163	9	AL645821	AL645821	Human DNA
584	206.2	22.7	13703	9	AC020982	657	205.8	22.7	97075	9	AC010289	AC010289	Homo sapi
585	206.2	22.7	147102	9	AC002476	658	205.8	22.7	110000	2	BX276116_04	AB020878	Human DNA
586	206.2	22.7	149181	2	AL357078	659	205.8	22.7	110455	9	AL353141	AL353141	Human DNA
587	206.2	22.7	157442	9	AC021813	660	205.8	22.7	118873	9	HS118484	AL034450	Human DNA
588	206.2	22.7	157442	9	AC105001	661	205.8	22.7	119631	9	AC008888	AC008888	Homo sapi
589	206.2	22.7	158608	9	CNS05TDJ	662	205.8	22.7	130403	9	AL158139	AL158139	Human DNA
590	206.2	22.7	161970	9	AP005660	663	205.8	22.7	137022	9	AC104231	AC104231	Homo sapi
591	206.2	22.7	162245	9	AC011008	664	205.8	22.7	139072	9	AP000485	AP000485	Homo sapi
592	206.2	22.7	163444	2	AC025866	665	205.8	22.7	139072	9	AC007952	AC007952	Homo sapi
593	206.2	22.7	164168	9	AL135927	666	205.8	22.7	140176	2	AC162725	AC162725	Human DNA
594	206.2	22.7	164179	9	AC0072227	667	205.8	22.7	143223	2	AC016411	AL162725	Human DNA
595	206.2	22.7	170107	2	AC151445	668	205.8	22.7	146515	2	AC146981	AC146981	Homo sapi
596	206.2	22.7	171467	9	AL449223	669	205.8	22.7	155567	2	AC073492	AC073492	Homo sapi
597	206.2	22.7	171627	9	AL662797	670	205.8	22.7	157813	2	AC015957	AC015957	Homo sapi
598	206.2	22.7	175945	2	AC022147	671	205.8	22.7	158103	9	AC007952	AC007952	Homo sapi
599	206.2	22.7	179146	2	AC067852	672	205.8	22.7	162337	2	CNS01D1Y	AL133378	Human chr
600	206.2	22.7	179854	2	AC149445	673	205.8	22.7	162943	9	AC092938	AC092938	Homo sapi
601	206.2	22.7	180347	2	AC009415	674	205.8	22.7	164725	9	AP005118	AP005118	Homo sapi
602	206.2	22.7	184557	2	AC149554	675	205.8	22.7	166857	9	AC019160	AC019160	Homo sapi
603	206.2	22.7	185617	9	AL662848	676	205.8	22.7	168064	2	AC019160	AC019160	Homo sapi

C 677	205.8	22.7	169064	2	AC023767	AC023767 Homo sapi	C 750	205.6	22.7	193643	9	AC018644	AC018644 Homo sapi
C 678	205.8	22.7	169979	2	AC013700	AC013700 Homo sapi	C 751	205.6	22.7	197000	9	AC124859	AC124859 Homo sapi
C 679	205.8	22.7	171812	2	AC013389	AC013389 Homo sapi	C 752	205.6	22.7	202815	2	AP267169	AP267169 Homo sapi
C 680	205.8	22.7	174839	9	AL157335	AL157335 Human DNA	C 753	205.6	22.7	209859	9	AC084083	AC084083 Homo sapi
C 681	205.8	22.7	175195	2	AP001319	AP001319 Homo sapi	C 754	205.6	22.7	209870	9	AC104431	AC104431 Homo sapi
C 682	205.8	22.7	178336	2	AC060768	AC060768 Homo sapi	C 755	205.6	22.7	215150	9	AC026689	AC026689 Homo sapi
C 683	205.8	22.7	178625	2	AC106017	AC106017 Homo sapi	C 756	205.6	22.7	218074	9	AC023283	AC023283 Homo sapi
C 684	205.8	22.7	178975	2	AC023222	AC023222 Homo sapi	C 757	205.6	22.7	218630	2	AC145892	AC145892 Pan trogl
C 685	205.8	22.7	179272	2	AC069149	AC069149 Homo sapi	C 758	205.6	22.7	220458	2	AC010320	AC010320 Homo sapi
C 686	205.8	22.7	179372	2	AC040922	AC040922 Homo sapi	C 759	205.6	22.7	278310	2	AC069592	AC069592 Homo sapi
C 687	205.8	22.7	179511	2	AC025283	AC025283 Homo sapi	C 760	205.4	22.6	2819	6	AX330468	AX330468 Sequence
C 688	205.8	22.7	179581	2	AC009397	AC009397 Homo sapi	C 761	205.4	22.6	32638	2	AC146707	AC146707 Homo sapi
C 689	205.8	22.7	182301	2	AC012498	AC012498 Homo sapi	C 762	205.4	22.6	41385	9	AC144836	AC144836 Homo sapi
C 690	205.8	22.7	182431	2	AC068380	AC068380 Homo sapi	C 763	205.4	22.6	56516	6	BD196412	BD196412 Prostatic
C 691	205.8	22.7	186115	2	AC008474	AC008474 Homo sapi	C 764	205.4	22.6	56520	6	BD196564	BD196564 Prostatic
C 692	205.8	22.7	188100	2	AC134780	AC134780 Homo sapi	C 765	205.4	22.6	62799	2	AC114687	AC114687 Homo sapi
C 693	205.8	22.7	188460	2	AC010542	AC010542 Homo sapi	C 766	205.4	22.6	81403	2	AC092849	AC092849 Homo sapi
C 694	205.8	22.7	188560	2	AC141415	AC141415 Pan trogl	C 767	205.4	22.6	95360	2	AC022465	AC022465 Homo sapi
C 695	205.8	22.7	190025	2	AC140145	AC140145 Homo sapi	C 768	205.4	22.6	96594	6	AX695779	AX695779 Sequence
C 696	205.8	22.7	193312	2	AP004370	AP004370 Homo sapi	C 769	205.4	22.6	96865	2	AC138684	AC138684 Homo sapi
C 697	205.8	22.7	193390	2	AC013730	AC013730 Homo sapi	C 770	205.4	22.6	100259	9	AC005800	AC005800 Homo sapi
C 698	205.8	22.7	194237	2	AC068870	AC068870 Homo sapi	C 771	205.4	22.6	102202	9	AC027694	AC027694 Homo sapi
C 699	205.8	22.7	194237	9	AC107943	AC107943 Homo sapi	C 772	205.4	22.6	104726	9	AC008087	AC008087 Homo sapi
C 700	205.8	22.7	195110	9	AL954236	AL954236 Pan trogl	C 773	205.4	22.6	109238	9	AC004997	AC004997 Homo sapi
C 701	205.8	22.7	198664	9	AP006256	AP006256 Homo sapi	C 774	205.4	22.6	116470	9	AC099568	AC099568 Homo sapi
C 702	205.8	22.7	207901	2	AC147043	AC147043 Pan trogl	C 775	205.4	22.6	118234	9	AL355476	AL355476 Human DNA
C 703	205.8	22.7	211305	9	AC079988	AC079988 Homo sapi	C 776	205.4	22.6	126327	9	AC005252	AC005252 Homo sapi
C 704	205.8	22.7	231190	9	CNS01D03	AL131353 Human chr	C 777	205.4	22.6	127006	9	AL138849	AL138849 Human DNA
C 705	205.8	22.7	257967	2	AL365337	AL365337 Mus muscu	C 778	205.4	22.6	129293	9	HS1178N10	HS1178N10 Human
C 706	205.8	22.7	297235	2	AL499603	AL499603 Homo sapi	C 779	205.4	22.6	130282	2	AC1078973	AC1078973 Homo sapi
C 707	205.6	22.7	401	11	BV190685	BV190685 sqm16804	C 780	205.4	22.6	130445	9	AC005186	AC005186 Homo sapi
C 708	205.6	22.7	482	9	AV190788	AV190788 Porco ptyg	C 781	205.4	22.6	134471	9	AC005186	AC005186 Homo sapi
C 709	205.6	22.7	40649	2	AC003111	AC003111 Human DNA	C 782	205.4	22.6	139376	9	HS095742	HS095742 Human
C 710	205.6	22.7	45459	2	AC006103	AC006103 Homo sapi	C 783	205.4	22.6	142201	9	AC124248	AC124248 Homo sapi
C 711	205.6	22.7	75237	2	AC022935	AC022935 Homo sapi	C 784	205.4	22.6	143146	9	AC079855	AC079855 Homo sapi
C 712	205.6	22.7	83969	2	AC005210	AC005210 c1c1b_179	C 785	205.4	22.6	150563	2	AL161444	AL161444 Human DNA
C 713	205.6	22.7	110000	2	AL732359_00	AL732359 Homo sapi	C 786	205.4	22.6	155369	2	AC084228	AC084228 Homo sapi
C 714	205.6	22.7	110000	2	AL732359_01	Continuation (2 of	C 787	205.4	22.6	155989	2	AL354932	AL354932 Human DNA
C 715	205.6	22.7	115043	9	AL663070	AL663070 Human DNA	C 788	205.4	22.6	157676	2	AC027358	AC027358 Homo sapi
C 716	205.6	22.7	118405	9	AC012349	AC012349 Homo sapi	C 789	205.4	22.6	158257	9	AC005585	AC005585 Homo sapi
C 717	205.6	22.7	131140	2	AC027474	AC027474 Homo sapi	C 790	205.4	22.6	159322	2	AC026085	AC026085 Homo sapi
C 718	205.6	22.7	131747	9	AC124857	AC124857 Homo sapi	C 791	205.4	22.6	159978	2	AC139479	AC139479 Homo sapi
C 719	205.6	22.7	134960	2	AP002337	AP002337 Homo sapi	C 792	205.4	22.6	161309	9	AC100839	AC100839 Homo sapi
C 720	205.6	22.7	137233	2	AC090221	AC090221 Homo sapi	C 793	205.4	22.6	164026	2	AC143349	AC143349 Homo sapi
C 721	205.6	22.7	141007	2	AC025764	AC025764 Homo sapi	C 794	205.4	22.6	165307	2	AC148831	AC148831 Pan trogl
C 722	205.6	22.7	142520	9	HS6208E1	AL031667 Human DNA	C 795	205.4	22.6	165307	2	AC148831	AC148831 Pan trogl
C 723	205.6	22.7	151450	9	AC108679	AC108679 Homo sapi	C 796	205.4	22.6	165799	2	AC100813	AC100813 Homo sapi
C 724	205.6	22.7	151452	2	AP001894	AP001894 Homo sapi	C 797	205.4	22.6	165807	2	AL391810	AL391810 Homo sapi
C 725	205.6	22.7	152484	2	AC067992	AC067992 Homo sapi	C 798	205.4	22.6	167005	2	AC009822	AC009822 Homo sapi
C 726	205.6	22.7	153185	2	AC073228	AC073228 Homo sapi	C 799	205.4	22.6	167075	2	AC138885	AC138885 Homo sapi
C 727	205.6	22.7	155290	9	AL359175	AL359175 Human DNA	C 800	205.4	22.6	168136	2	AP287957	AP287957 Homo sapi
C 728	205.6	22.7	160370	9	AC023464	AC023464 Homo sapi	C 801	205.4	22.6	169371	2	AC138902	AC138902 Homo sapi
C 729	205.6	22.7	170797	9	AC011379	AC011379 Homo sapi	C 802	205.4	22.6	169414	2	AC068707	AC068707 Homo sapi
C 730	205.6	22.7	170849	9	AC126366	AC126366 Homo sapi	C 803	205.4	22.6	169665	2	AC144566	AC144566 Homo sapi
C 731	205.6	22.7	172837	2	AL450304	AL450304 Human DNA	C 804	205.4	22.6	170135	2	AC137873	AC137873 Homo sapi
C 732	205.6	22.7	174856	2	BX296555	BX296555 Homo sapi	C 805	205.4	22.6	172334	2	AC010650	AC010650 Homo sapi
C 733	205.6	22.7	175006	2	AC027589	AC027589 Homo sapi	C 806	205.4	22.6	172812	9	AC016903	AC016903 Homo sapi
C 734	205.6	22.7	176278	9	AC024028	AC024028 Homo sapi	C 807	205.4	22.6	172827	9	AC007216	AC007216 Homo sapi
C 735	205.6	22.7	176550	9	AL356336	AL356336 Human DNA	C 808	205.4	22.6	173525	2	AC067893	AC067893 Homo sapi
C 736	205.6	22.7	178653	2	AC090088	AC090088 Homo sapi	C 809	205.4	22.6	177483	9	AC068233	AC068233 Homo sapi
C 737	205.6	22.7	178982	2	AP001591	AP001591 Homo sapi	C 810	205.4	22.6	180221	9	AC007277	AC007277 Homo sapi
C 738	205.6	22.7	179627	2	AC113426	AC113426 Homo sapi	C 811	205.4	22.6	180392	2	AC192939	AC192939 Homo sapi
C 739	205.6	22.7	179666	2	AC138145	AC138145 Homo sapi	C 812	205.4	22.6	181277	2	AC139478	AC139478 Homo sapi
C 740	205.6	22.7	180889	2	AC079986	AC079986 Homo sapi	C 813	205.4	22.6	181597	9	AC090515	AC090515 Homo sapi
C 741	205.6	22.7	184057	9	AP000753	AP000753 Homo sapi	C 814	205.4	22.6	182092	9	AC013477	AC013477 Homo sapi
C 742	205.6	22.7	184059	2	AC090382	AC090382 Homo sapi	C 815	205.4	22.6	183307	9	AC096539	AC096539 Homo sapi
C 743	205.6	22.7	184512	9	AC079804	AC079804 Homo sapi	C 816	205.4	22.6	183485	2	AC022578	AC022578 Homo sapi
C 744	205.6	22.7	184840	9	AC079907	AC079907 Homo sapi	C 817	205.4	22.6	183861	9	AC078816	AC078816 Homo sapi
C 745	205.6	22.7	184886	9	AC005358	AC005358 Homo sapi	C 818	205.4	22.6	184148	2	AC148725	AC148725 Homo sapi
C 746	205.6	22.7	184889	9	AL442125	AL442125 Human DNA	C 819	205.4	22.6	184585	2	AC079465	AC079465 Homo sapi
C 747	205.6	22.7	185242	2	AC084709	AC084709 Homo sapi	C 820	205.4	22.6	184649	2	AC025185	AC025185 Homo sapi
C 748	205.6	22.7	191291	2	AC148313	AC148313 Pan trogl	C 821	205.4	22.6	185182	9	AC093423	AC093423 Homo sapi
C 749	205.6	22.7	192203	9	AC034102	AC034102 Homo sapi	C 822	205.4	22.6	185834	2	AC009632	AC009632 Homo sapi

823	205.4	22.6	185964	9	AC009339	AC009339	Homo sapi
824	205.4	22.6	186212	2	AC006938	AC006938	Homo sapi
825	205.4	22.6	189579	9	AL1354733	AL1354733	Human DNA
826	205.4	22.6	190483	2	AC148839	AC148839	Pan trogl
827	205.4	22.6	191279	2	AL1590872	AL1590872	Homo sapi
828	205.4	22.6	192126	9	DJ720M14	DJ720M14	Human DNA
829	205.4	22.6	196337	9	AL1358975	AL1358975	Human DNA
830	205.4	22.6	196421	2	AC0090780	AC0090780	Homo sapi
831	205.4	22.6	199079	2	AC097267	AC097267	Pan trogl
832	205.4	22.6	199230	2	AC048360	AC048360	Homo sapi
833	205.4	22.6	199454	2	AC117180	AC117180	Homo sapi
834	205.4	22.6	202768	2	AC092345	AC092345	Homo sapi
835	205.4	22.6	204963	2	AC145617	AC145617	Homo sapi
836	205.4	22.6	206737	9	AC126917	AC126917	Homo sapi
837	205.4	22.6	209718	2	AC091099	AC091099	Homo sapi
838	205.4	22.6	210688	2	AC137498	AC137498	Homo sapi
839	205.4	22.6	210867	2	AC144878	AC144878	Pongo pyg
840	205.4	22.6	213481	9	AC134618	AC134618	Homo sapi
841	205.4	22.6	213481	9	AC134618	AC134618	Homo sapi
842	205.4	22.6	225116	9	AC134619	AC134619	Homo sapi
843	205.4	22.6	225116	9	AC134619	AC134619	Homo sapi
844	205.4	22.6	231234	2	AL1591116	AL1591116	Homo sapi
845	205.4	22.6	237952	2	AL1591116	AL1591116	Homo sapi
846	205.4	22.6	248344	2	AC134883	AC134883	Homo sapi
847	205.4	22.6	328187	2	AC117393	AC117393	Homo sapi
848	205.2	22.6	301	6	AX741028	AX741028	Sequence
849	205.2	22.6	3674	9	AF517523	AF517523	Homo sapi
850	205.2	22.6	32351	9	HUMHDC	HUMHDC	Homo sapien
851	205.2	22.6	73845	2	AL1356478	AL1356478	Homo sapi
852	205.2	22.6	85138	9	AL137224	AL137224	Human DNA
853	205.2	22.6	88215	9	AC006963	AC006963	Homo sapi
854	205.2	22.6	95240	9	AC026718	AC026718	Homo sapi
855	205.2	22.6	111321	2	AC026718	AC026718	Homo sapi
856	205.2	22.6	110825	9	AC010469	AC010469	Homo sapi
857	205.2	22.6	123221	9	AC011472	AC011472	Homo sapi
858	205.2	22.6	124949	9	AL1358794	AL1358794	Human DNA
859	205.2	22.6	126380	2	AP000714	AP000714	Homo sapi
860	205.2	22.6	129169	2	AC032038	AC032038	Homo sapi
861	205.2	22.6	142273	9	AL1391994	AL1391994	Human DNA
862	205.2	22.6	142813	2	AC090624	AC090624	Homo sapi
863	205.2	22.6	143790	2	AC055811	AC055811	Homo sapi
864	205.2	22.6	153223	2	AC074339	AC074339	Homo sapi
865	205.2	22.6	153385	2	AC019355	AC019355	Homo sapi
866	205.2	22.6	159840	2	AP000869	AP000869	Homo sapi
867	205.2	22.6	163115	2	AC105902	AC105902	Homo sapi
868	205.2	22.6	165531	2	AC023038	AC023038	Homo sapi
869	205.2	22.6	167628	9	AC092570	AC092570	Homo sapi
870	205.2	22.6	170269	9	AC090307	AC090307	Homo sapi
871	205.2	22.6	172876	9	AC114489	AC114489	Homo sapi
872	205.2	22.6	173836	2	AP001404	AP001404	Homo sapi
873	205.2	22.6	173977	9	AC010170	AC010170	Homo sapi
874	205.2	22.6	174559	9	AC015720	AC015720	Homo sapi
875	205.2	22.6	174724	2	AC140096	AC140096	Pan trogl
876	205.2	22.6	175028	2	AC066692	AC066692	Homo sapi
877	205.2	22.6	178902	2	AL151525	AL151525	Human sapi
878	205.2	22.6	178985	9	HS340B19	HS340B19	Human DNA
879	205.2	22.6	179221	9	AC114493	AC114493	Homo sapi
880	205.2	22.6	185167	9	AC009077	AC009077	Homo sapi
881	205.2	22.6	191594	9	AC130462	AC130462	Homo sapi
882	205.2	22.6	194156	2	AC009851	AC009851	Homo sapi
883	205.2	22.6	197215	2	AP002954	AP002954	Homo sapi
884	205.2	22.6	198410	2	AP000831	AP000831	Homo sapi
885	205.2	22.6	199321	2	AP000941	AP000941	Homo sapi
886	205.2	22.6	201981	2	AC073640	AC073640	Homo sapi
887	205.2	22.6	204001	2	AC087783	AC087783	Homo sapi
888	205.2	22.6	204480	2	AC019083	AC019083	Homo sapi
889	205.2	22.6	204769	2	AC150377	AC150377	Callithrix
890	205.2	22.6	213025	2	AC021159	AC021159	Homo sapi
891	205.2	22.6	242913	9	AC115994	AC115994	Homo sapi
892	205.2	22.6	16765	9	AL1732409	AL1732409	Human DNA
893	205	22.6	16765	9	AL1732409	AL1732409	Human DNA
894	205	22.6	16765	9	AL1732409	AL1732409	Human DNA
895	205	22.6	82251	9	AC004506	AC004506	Homo sapi
896	205	22.6	84678	2	AC087464	AC087464	Homo sapi
897	205	22.6	88018	9	AC010418	AC010418	Homo sapi
898	205	22.6	90096	9	AL611925	AL611925	Human DNA
899	205	22.6	91224	9	AC093582	AC093582	Homo sapi
900	205	22.6	94168	9	AL133415	AL133415	Human DNA
901	205	22.6	94635	9	AC139931	AC139931	Homo sapi
902	205	22.6	95855	9	HSAC000115	HSAC000115	Human BAC
903	205	22.6	98876	9	AC009488	AC009488	Homo sapi
904	205	22.6	105787	9	AC113367	AC113367	Homo sapi
905	205	22.6	107842	9	AC093859	AC093859	Homo sapi
906	205	22.6	109761	9	AF271405	AF271405	Homo sapi
907	205	22.6	112351	9	AC001484	AC001484	Homo sapi
908	205	22.6	115888	9	AC006015	AC006015	Homo sapi
909	205	22.6	115888	9	AC002468	AC002468	Human Chr
910	205	22.6	123004	9	HS196823	HS196823	Human DNA
911	205	22.6	123657	9	HS1097814	HS1097814	Human DNA
912	205	22.6	124437	9	AL139125	AL139125	Human DNA
913	205	22.6	125495	9	AL135914	AL135914	Human DNA
914	205	22.6	129149	9	HS510D11	HS510D11	Human DNA
915	205	22.6	132414	2	AL1359882	AL1359882	Homo sapi
916	205	22.6	132916	9	AC018765	AC018765	Homo sapi
917	205	22.6	133154	9	HSBD90K10	HSBD90K10	Human DNA
918	205	22.6	135894	9	AC145425	AC145425	Homo sapi
919	205	22.6	144859	9	AC104997	AC104997	Homo sapi
920	205	22.6	145201	9	AC084854	AC084854	Homo sapi
921	205	22.6	146551	9	AC112249	AC112249	Homo sapi
922	205	22.6	147999	2	AL161635	AL161635	Homo sapi
923	205	22.6	150720	2	AL1513016	AL1513016	Human DNA
924	205	22.6	153486	2	AC063923	AC063923	Homo sapi
925	205	22.6	154386	2	AC016314	AC016314	Homo sapi
926	205	22.6	155382	2	AC127520	AC127520	Homo sapi
927	205	22.6	156581	2	AC145424	AC145424	Homo sapi
928	205	22.6	156589	2	HS537K23	HS537K23	Human DNA
929	205	22.6	157515	2	AL1391598	AL1391598	Homo sapi
930	205	22.6	159699	2	AC026833	AC026833	Homo sapi
931	205	22.6	160133	2	AC024355	AC024355	Homo sapi
932	205	22.6	160878	2	AC016971	AC016971	Homo sapi
933	205	22.6	162658	2	AC018617	AC018617	Homo sapi
934	205	22.6	162840	2	AC046203	AC046203	Homo sapi
935	205	22.6	166987	2	AL591434	AL591434	Homo sapi
936	205	22.6	168015	2	AP002007	AP002007	Homo sapi
937	205	22.6	168922	9	CNS01DPT	CNS01DPT	Human chr
938	205	22.6	170125	9	AC024082	AC024082	Homo sapi
939	205	22.6	171867	2	AC073394	AC073394	Homo sapi
940	205	22.6	173515	2	AC024553	AC024553	Homo sapi
941	205	22.6	173748	2	AP000788	AP000788	Homo sapi
942	205	22.6	175419	2	AP000907	AP000907	Homo sapi
943	205	22.6	180104	9	DJ526N18	DJ526N18	Homo sapi
944	205	22.6	180365	9	AC046143	AC046143	Homo sapi
945	205	22.6	186291	9	PTB083D21	PTB083D21	Pan trogl
946	205	22.6	186825	9	AC145984	AC145984	Homo sapi
947	205	22.6	188235	9	AC098869	AC098869	Homo sapi
948	205	22.6	188295	9	AC122133	AC122133	Homo sapi
949	205	22.6	191330	9	AC055271	AC055271	Homo sapi
950	205	22.6	191433	9	AC069152	AC069152	Homo sapi
951	205	22.6	191433	9	AF053356	AF053356	Homo sapi
952	205	22.6	227968	9	AF205588	AF205588	Homo sapi
953	205	22.6	312283	9	HS2MPO6	HS2MPO6	Human thymo
954	204.8	22.6	32234	9	AC092316	AC092316	Homo sapi
955	204.8	22.6	36246	9	AC114729	AC114729	Homo sapi
956	204.8	22.6	46894	9	AC114729	AC114729	Homo sapi
957	204.8	22.6	68003	2	BX333853	BX333853	Homo sapi
958	204.8	22.6	68617	2	AC0118659	AC0118659	Homo sapi
959	204.8	22.6	69912	2	AC010322	AC010322	Homo sapi
960	204.8	22.6	100130	9	AC090454	AC090454	Homo sapi
961	204.8	22.6	102387	9	AC022114	AC022114	Homo sapi
962	204.8	22.6	104941	9	AL1589663	AL1589663	Human DNA
963	204.8	22.6	108316	2	AX647597	AX647597	Sequence
964	204.8	22.6	110000	6	AL1390202	AL1390202	Continuation (6 of
965	204.8	22.6	116506	9	AL160163	AL160163	Human DNA
966	204.8	22.6	122292	9	AC013418	AC013418	Homo sapi
967	204.8	22.6	126080	9	AY029472	AY029472	Homo sapi
968	204.8	22.6	127399	9	AL158825	AL158825	Human DNA

969	204.8	22.6	135311	9	AC008798	Homo sapi	1042	204.6	22.6	173618	2	AC019045	Homo sapi
970	204.8	22.6	135618	2	AL359965	Homo sapi	c1043	204.6	22.6	174387	9	AC092350	Homo sapi
c 971	204.8	22.6	136002	9	AL3120024	Homo sapi	1044	204.6	22.6	177180	9	AC097384	Human DNA
c 972	204.8	22.6	142273	9	AL3191994	Human DNA	1045	204.6	22.6	179607	2	AC027272	Homo sapi
c 973	204.8	22.6	147514	9	AC008521	Homo sapi	c1046	204.6	22.6	183894	9	AC040970	Homo sapi
c 974	204.8	22.6	155452	9	AL049646	Human DNA	c1047	204.6	22.6	191824	9	AL161935	Human DNA
c 975	204.8	22.6	159791	9	HS0568F9	Human DNA	1048	204.6	22.6	192409	2	AC072033	Homo sapi
976	204.8	22.6	160850	9	AC009951	Homo sapi	1049	204.6	22.6	192898	9	AC145968	Homo sapi
c 977	204.8	22.6	165920	9	AC130184	Macaca mu	c1050	204.6	22.6	197630	9	AC015676	Homo sapi
c 978	204.8	22.6	168727	9	AC010222	Homo sapi	1051	204.6	22.6	197752	2	AC145130	Homo sapi
c 979	204.8	22.6	168931	2	AC118658	Homo sapi	c1052	204.6	22.6	198470	9	AC046170	Homo sapi
c 980	204.8	22.6	169193	2	AC144998	Pan trogl	1053	204.6	22.6	198564	9	AC008561	Homo sapi
c 981	204.8	22.6	169908	2	AC068523	Homo sapi	c1054	204.6	22.6	200420	9	AC138645	Homo sapi
c 982	204.8	22.6	170423	9	AC150910	Pan trogl	1055	204.6	22.6	200594	9	AC093117	Homo sapi
c 983	204.8	22.6	170423	9	AC018663	Human Chr	1056	204.6	22.6	200594	9	AC005632	Homo sapi
c 984	204.8	22.6	174378	9	AC020983	Homo sapi	c1057	204.6	22.6	203790	9	AC010422	Homo sapi
c 985	204.8	22.6	174902	2	AC110071	Homo sapi	c1058	204.6	22.6	207131	2	AC144876	Homo sapi
c 986	204.8	22.6	175075	9	AC113346	Homo sapi	c1059	204.6	22.6	210949	2	AC146885	Callithr
c 987	204.8	22.6	177750	9	AP005230	Homo sapi	1060	204.6	22.6	212426	9	AC104335	Homo sapi
c 988	204.8	22.6	177864	9	AC005874	Human Chr	1061	204.6	22.6	212426	9	AC012183	Homo sapi
c 989	204.8	22.6	177978	9	AP134471	Human Chr	c1062	204.6	22.6	220173	9	AC012183	Homo sapi
c 990	204.8	22.6	177978	9	AC009073	Homo sapi	1063	204.6	22.6	221484	2	AC144877	Pongo pyg
c 991	204.8	22.6	179798	9	AC009126	Homo sapi	1064	204.6	22.6	222085	2	AC144878	Gorilla g
c 992	204.8	22.6	181923	9	AC022872	Homo sapi	1065	204.6	22.6	226696	9	AC139026	Homo sapi
c 993	204.8	22.6	184948	2	AC009659	Homo sapi	c1066	204.6	22.6	248281	9	AC008737	Homo sapi
c 994	204.8	22.6	186047	9	AC074257	Homo sapi	1067	204.6	22.6	257700	2	AC147391	Pan trogl
c 995	204.8	22.6	189533	9	AC025678	Homo sapi	c1068	204.6	22.6	281662	2	AC117374	Homo sapi
c 996	204.8	22.6	192046	9	AC146459	Pan trogl	1069	204.6	22.6	300050	9	AB100084	Pan trogl
c 997	204.8	22.6	193101	2	AC110772	Homo sapi	c1070	204.4	22.5	6870	9	HM01111A	Human inter
c 998	204.8	22.6	195646	2	AC009561	Homo sapi	1071	204.4	22.5	8000	9	AF361481	Homo sapi
c 999	204.8	22.6	202041	2	AC093709	Pan trogl	c1072	204.4	22.5	11190	9	AY207429	Homo sapi
c1000	204.8	22.6	215422	9	AC007427	Homo sapi	1073	204.4	22.5	11954	9	AY587020	Homo sapi
c1001	204.8	22.6	230552	9	U66060	Human germ	c1074	204.4	22.5	11954	9	AL133275	Human DNA
c1002	204.8	22.6	232630	9	AC005098	Homo sapi	c1075	204.4	22.5	16242	9	AL136091	Human DNA
c1003	204.6	22.6	26096	9	U66061	Human germ	c1076	204.4	22.5	29186	9	AL357560	Human DNA
c1004	204.6	22.6	31215	9	AL160055	Human DNA	c1077	204.4	22.5	33550	9	AC003004	Human Chr
c1005	204.6	22.6	41026	9	AL158815	Human DNA	1078	204.4	22.5	44401	9	BX000360	Human DNA
c1006	204.6	22.6	68774	9	AC131159	Homo sapi	1079	204.4	22.5	67581	2	AL662859	Human DNA
c1007	204.6	22.6	80878	9	AY430083	Homo sapi	1080	204.4	22.5	90103	2	AC027802	Homo sapi
c1008	204.6	22.6	85763	9	AL359455	Human DNA	1081	204.4	22.5	92058	9	CR788295	Danio rer
c1009	204.6	22.6	100190	9	AC061992	Homo sapi	c1082	204.4	22.5	93634	2	BX119924	Human DNA
c1010	204.6	22.6	102517	2	AP002876	Homo sapi	1083	204.4	22.5	99249	9	AC127088	Homo sapi
c1011	204.6	22.6	1103875	9	AL136223	Human DNA	1084	204.4	22.5	100562	9	AL161916	Human DNA
c1012	204.6	22.6	11074	9	AC007569	Homo sapi	1085	204.4	22.5	102479	9	AL355870	Human DNA
c1013	204.6	22.6	112351	9	AC011484	Homo sapi	1086	204.4	22.5	103158	9	AC115107	Homo sapi
c1014	204.6	22.6	113916	9	AC003007	Human Chr	1087	204.4	22.5	105362	9	AL662871	Human DNA
c1015	204.6	22.6	114340	9	AL358232	Human DNA	1088	204.4	22.5	106928	9	AC012370	Homo sapi
c1016	204.6	22.6	116451	9	AL355860	Human DNA	c1089	204.4	22.5	106954	9	AC005049	Homo sapi
c1017	204.6	22.6	122764	9	HS0831D17	Human DNA	1090	204.4	22.5	107526	9	AC104651	Homo sapi
c1018	204.6	22.6	125579	9	AL161772	Human DNA	1091	204.4	22.5	108048	9	HS111M5	Human DNA
c1019	204.6	22.6	129441	9	AL136170	Human DNA	1092	204.4	22.5	111651	9	AC115108	Homo sapi
c1020	204.6	22.6	140800	2	AC018332	Homo sapi	1093	204.4	22.5	112453	6	CR626938	Human DNA
c1021	204.6	22.6	145190	2	AC008730	Homo sapi	c1094	204.4	22.5	112973	9	CR847517	Human DNA
c1022	204.6	22.6	148131	9	AC109489	Homo sapi	1095	204.4	22.5	117051	9	AC115106	Homo sapi
c1023	204.6	22.6	148285	2	AL451053	Homo sapi	1096	204.4	22.5	117838	9	AC010463	Homo sapi
c1024	204.6	22.6	150714	2	AC090278	Homo sapi	1097	204.4	22.5	127661	9	AC006014	Homo sapi
c1025	204.6	22.6	151329	9	AP188030	Homo sapi	c1098	204.4	22.5	128736	9	CR812473	Human DNA
c1026	204.6	22.6	152824	9	AC107072	Homo sapi	c1099	204.4	22.5	133378	9	AC090398	Homo sapi
c1027	204.6	22.6	154158	2	AL365257	Homo sapi	c1100	204.4	22.5	134793	9	AC020922	Homo sapi
c1028	204.6	22.6	158617	9	AC135972	Homo sapi	1101	204.4	22.5	147233	2	AC087486	Homo sapi
c1029	204.6	22.6	159597	9	AC008747	Homo sapi	c1102	204.4	22.5	147885	2	AL353793	Homo sapi
c1030	204.6	22.6	159989	2	AC138687	Homo sapi	1103	204.4	22.5	154251	2	AC116974	Homo sapi
c1031	204.6	22.6	159988	2	AC074282	Homo sapi	c1104	204.4	22.5	156595	2	AC147378	Homo sapi
c1032	204.6	22.6	161492	9	AC007780	Homo sapi	1105	204.4	22.5	156889	2	AC004586	Homo sapi
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c1035	204.6	22.6	166553	2	AL844523	Homo sapi	1108	204.4	22.5	160426	2	AC087697	Homo sapi
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c1038	204.6	22.6	167110	2	AC022621	Homo sapi	c1111	204.4	22.5	162445	2	AC022488	Homo sapi
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c1040	204.6	22.6	170705	9	AC013459	Homo sapi	1113	204.4	22.5	165382	2	AC024408	Homo sapi
c1041	204.6	22.6	171477	9	AC026457	Homo sapi	1114	204.4	22.5	167286	2	AP001638	Homo sapi

c1115	204.4	22.5	168145	9	AL159171	Human DNA
1116	204.4	22.5	169059	2	AC009790	Homo sapi
c1117	204.4	22.5	169439	9	AC008021	Homo sapi
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c1119	204.4	22.5	170655	2	AP001012	Homo sapi
1120	204.4	22.5	172551	2	AP001405	Homo sapi
c1121	204.4	22.5	172883	2	AP003967	Homo sapi
1122	204.4	22.5	173058	9	AC104564	Homo sapi
c1123	204.4	22.5	175872	9	AP001266	Homo sapi
1124	204.4	22.5	177411	9	AC005696	Homo sapi
1125	204.4	22.5	177951	2	AC074383	Homo sapi
c1126	204.4	22.5	178029	9	AC106037	Homo sapi
c1127	204.4	22.5	178066	9	AC087641	Homo sapi
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1131	204.4	22.5	183085	9	AC005815	Homo sapi
1132	204.4	22.5	183779	9	AC005488	Homo sapi
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c1140	204.4	22.5	197807	2	AC147057	Homo sapi
c1141	204.4	22.5	201093	2	AC144750	pan trogl
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c1143	204.4	22.5	203050	2	HS44N10	
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1145	204.4	22.5	210608	9	AC006028	Homo sapi
c1146	204.4	22.5	212237	9	AC079235	Homo sapi
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1150	204.4	22.5	235313	2	AC148034	Homo sapi
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1152	204.2	22.5	2748	9	AC004124	Homo sapi
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c1159	204.2	22.5	26013	9	AC142230	Homo sapi
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1161	204.2	22.5	34551	9	BX248518	Human DNA
1162	204.2	22.5	39000	9	AC004322	Genomic B
1163	204.2	22.5	39634	2	AC139315	Homo sapi
1164	204.2	22.5	39816	2	AL954350	Continuation (6 of
c1165	204.2	22.5	40948	9	AC140106	Homo sapi
c1166	204.2	22.5	43600	9	AC004209	Homo sapi
1167	204.2	22.5	44983	2	AC139093	Homo sapi
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1169	204.2	22.5	60563	2	AC137682	Homo sapi
1170	204.2	22.5	64172	2	BX000357	Human DNA
1171	204.2	22.5	70448	9	CR388372	Human DNA
1172	204.2	22.5	73641	2	CR758912	Human sapi
c1173	204.2	22.5	81195	9	AL627143	Human DNA
1174	204.2	22.5	82724	9	BX927220	Human DNA
c1175	204.2	22.5	95029	2	AL357492	Homo sapi
1176	204.2	22.5	95505	9	AL357934	Human DNA
c1177	204.2	22.5	100000	9	AP000514	Homo sapi
1178	204.2	22.5	102105	9	AL136166	Human DNA
c1179	204.2	22.5	107506	9	HS0472M2	Human DNA
1180	204.2	22.5	110000	2	AC117723	Continuation (2 of
1181	204.2	22.5	110000	2	BX576424	Continuation (5 of
1182	204.2	22.5	113066	2	AC026729	Homo sapi
c1183	204.2	22.5	113906	2	AC136589	Homo sapi
c1184	204.2	22.5	115793	9	AC104115	Homo sapi
1185	204.2	22.5	118504	9	AC094080	Homo sapi
1186	204.2	22.5	119847	9	AF064866	Homo sapi
1187	204.2	22.5	121930	2	CR762481	Homo sapi
c1188	204.2	22.5	122742	2	HS167P19	
c1189	204.2	22.5	123160	9	AL353719	Human DNA
1190	204.2	22.5	129203	9	AC104819	Homo sapi
c1191	204.2	22.5	129608	9	AL353685	Human DNA
1192	204.2	22.5	132521	9	AC008710	Homo sapi
c1193	204.2	22.5	133921	9	AC103587	Homo sapi
1194	204.2	22.5	134296	9	HS352H24	Homo sapi
c1195	204.2	22.5	134857	9	HS3930L11	Human DNA
1196	204.2	22.5	135964	9	AC005914	Homo sapi
c1197	204.2	22.5	137113	9	AC076966	Homo sapi
1198	204.2	22.5	143210	9	AC022407	Homo sapi
c1199	204.2	22.5	143969	9	AL357552	Human DNA
1200	204.2	22.5	144695	2	AC012438	Homo sapi
c1201	204.2	22.5	145253	9	AC006329	Homo sapi
c1202	204.2	22.5	149034	9	AP275948	Homo sapi
c1203	204.2	22.5	149249	9	AC079945	Homo sapi
c1204	204.2	22.5	149370	9	AC012626	Homo sapi
c1205	204.2	22.5	150485	2	AC012292	Homo sapi
1206	204.2	22.5	151328	9	AL662800	Human DNA
c1207	204.2	22.5	152556	9	CNS01DSY	pan trogl
c1208	204.2	22.5	152714	9	BS000156	Homo sapi
c1209	204.2	22.5	153609	9	HSAP9617	Homo sapi
c1210	204.2	22.5	154589	9	AC006557	Homo sapi
1211	204.2	22.5	155800	2	AC146667	Homo sapi
c1212	204.2	22.5	156043	2	AC013631	Homo sapi
c1213	204.2	22.5	156264	9	AC103921	Homo sapi
1214	204.2	22.5	157860	9	AL391241	Human DNA
c1215	204.2	22.5	158103	9	AC007952	Homo sapi
c1216	204.2	22.5	160012	2	AL136231	Human DNA
1217	204.2	22.5	160301	2	AC130417	Homo sapi
c1218	204.2	22.5	162948	2	AL662822	Human DNA
c1219	204.2	22.5	164282	2	AC015734	Homo sapi
1220	204.2	22.5	164958	9	AC099340	Homo sapi
c1221	204.2	22.5	165227	9	AC025884	Homo sapi
1222	204.2	22.5	168210	9	AC018719	Homo sapi
c1223	204.2	22.5	169460	9	AC104370	Homo sapi
1224	204.2	22.5	170048	2	AC025240	Homo sapi
c1225	204.2	22.5	170686	9	AC012595	Homo sapi
c1226	204.2	22.5	170797	9	AC011379	Homo sapi
1227	204.2	22.5	170803	2	AC016155	Homo sapi
c1228	204.2	22.5	170908	2	AC022557	Homo sapi
1229	204.2	22.5	171520	2	AP001637	Homo sapi
c1230	204.2	22.5	172676	9	AC015711	Homo sapi
1231	204.2	22.5	172883	9	AP003967	Homo sapi
c1232	204.2	22.5	173322	9	AC022168	Homo sapi
c1233	204.2	22.5	178184	2	AC008770	Homo sapi
1234	204.2	22.5	178184	9	AC020694	Homo sapi
c1235	204.2	22.5	180155	2	AC026556	Homo sapi
1236	204.2	22.5	182454	2	AP001004	Homo sapi
c1237	204.2	22.5	183689	2	AC146129	Homo sapi
c1238	204.2	22.5	183854	2	AC145951	Homo sapi
c1239	204.2	22.5	183959	6	AX092589	Sequence
c1240	204.2	22.5	184302	9	AL162393	Human DNA
1241	204.2	22.5	185463	9	AC016065	Homo sapi
c1242	204.2	22.5	186210	9	AC007596	Homo sapi
1243	204.2	22.5	187461	9	AL550453	Human DNA
c1244	204.2	22.5	188863	9	AC007345	Homo sapi
1245	204.2	22.5	191246	9	AC068769	Homo sapi
1246	204.2	22.5	191292	2	AC084420	Homo sapi
1247	204.2	22.5	192430	2	AC129804	Homo sapi
c1248	204.2	22.5	192853	2	AC147313	pan trogl
c1249	204.2	22.5	192971	9	AC040173	Homo sapi
c1250	204.2	22.5	194056	9	AL550708	Human DNA
c1251	204.2	22.5	194173	9	AL160231	Human chr
c1252	204.2	22.5	196037	9	AC129492	Homo sapi
c1253	204.2	22.5	197616	9	AC069113	Homo sapi
1254	204.2	22.5	199882	9	AL354720	Human DNA
c1255	204.2	22.5	201144	9	AF287252	Homo sapi
c1256	204.2	22.5	201197	2	HS424J12	Homo sapi
c1257	204.2	22.5	203330	2	AC136933	Homo sapi
c1258	204.2	22.5	204393	2	AC145989	pan trogl
c1259	204.2	22.5	205498	9	AC079416	Homo sapi
c1260	204.2	22.5	213611	9	AF276759	Homo sapi
c293014	Human sapien					
AL353719	Human DNA					
AC104819	Homo sapi					
AL353685	Human DNA					
AC008710	Homo sapi					
AC103587	Homo sapi					
AL449215	Homo sapi					
AL049759	Human DNA					
AC005914	Homo sapi					
AC076966	Homo sapi					
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AL357552	Human DNA					
AC012438	Homo sapi					
AC006329	Homo sapi					
AP275948	Homo sapi					
AC079945	Homo sapi					
AC012626	Homo sapi					
AC012292	Homo sapi					
AL662800	Human DNA					
AL122035	Human chr					
BS000156	pan trogl					
AJ009617	Homo sapi					
AC006557	Homo sapi					
AC146667	Homo sapi					
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AL391241	Human DNA					
AC007952	Homo sapi					
AL136231	Human DNA					
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AC018719	Homo sapi					
AC104370	Homo sapi					
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AC012595	Homo sapi					
AC011379	Homo sapi					
AC022168	Homo sapi					
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DEFINITION Sequence 97 from Patent WO0193983.
ACCESSION AX358844
VERSION AX358844.1 GI:18675323
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Baker, K.P., Deenoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0193983-A 97 13-DEC-2001;
Genentech Inc. (US)
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Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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DEFINITION Sequence 97 from Patent WO0208288.
ACCESSION AX362337
VERSION AX362337.1 GI:18694626
KEYWORDS
SOURCE Homo sapiens (human)

REFERENCE	ORGANISM
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Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godweli, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumetazoa; Eutheria; Primatea; Catarrhini; Hominidae; Homo.
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Genentech, Inc. (US)	
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Matches 907; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
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QY	841	TGCGGTGAGCCGAGATCGCGCGCTGATTTCCAGCCTTGAGCGACAAAGTGAAGATCCATC	900
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DEFINITION	Sequence 398 from Patent WO0073454.		
ACCESSION	AX403511		
VERSION	AX403511.1	GI:21436996	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
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TITLE	Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D., Ferrara, N., Gerber, H., Gettleisen, M., Goddard, A., Godwakt, P., Grimaldi, C.J., Gurney, A.L., Kijavlin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tamas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.		
JOURNAL	Secreted and transmembrane polypeptides and nucleic acids encoding the same Patent: WO 0073454-A 398 07-DEC-2000; Genentech Inc. (US)		
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QY	181	GAGAGAGTGTCTGGGTCAAGGAGCGCAGAGAGCGCTCAACAGCTCCAGCCCTTGTATAC	240
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QY	241	GAGAGACACATTTGGGACAGGTCCAGCGATGTGTCGGAGTCCACACACAGACTGGCGGAGG	300
DB	241	GAGAGACACATTTGGGACAGGTCCAGCGATGTGTCGGAGTCCACACACAGACTGGCGGAGG	300
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DB	301	GACAGAGGGGGACAGTTCTGTGTGCTTGGTTGACACATTAAGAGGGCTTGGCCAGTCCA	360
QY	361	GGGTGGGGGGCGGCAACTCCATTAAGAAACAGAGGGGTCTGGGCGCCCGGACAGAGTCA	420
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RESULT 5
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
Source

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AY358690.1 GI:37182501
FLI_CDNA.
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
1 (bases 1 to 907)
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowen,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
Schoenfeld,J., Seehagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagte,A., Vandlen,R., Watanabe,C., Wiand,D., Woods,K.,
Xie,M.H., Yamamura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Klodt,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
12975309
2 (bases 1 to 907)
Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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ORIGIN

Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 1e-244;
Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CCTAGGGGCTGGAATTTGCTGTTAACAAGATACCTAGGGGACAGCCCATAGGGGA 120
DB 61 CCTAGGGGCTGGAATTTGCTGTTAACAAGATACCTAGGGGACAGCCCATAGGGGA 120
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LOCUS	AC105210	101777 bp	DNA linear PRI 27-MAR-2003
DEFINITION	Homo sapiens chromosome 8, clone RP11-118P12, complete sequence.		
ACCESSION	AC105210		
VERSION	AC105210.10	GI:29294339	
KEYWORDS	HTC		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 101777)		
TITLE	Birtten,B., Nusbaum,C. and Lander,E.		
JOURNAL	Homo sapiens chromosome 8, clone RP11-118P12		
REFERENCE	2 (bases 1 to 101777)		
AUTHORS	Birtten,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N., Anderson,S., Barra,N., Bairsten,V., Boguslavsky,L., Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.Y., Chazaro,B., Choepe,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glade,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kelle,C., Lacroque,K., Lamasares,R., Landers,T., Lehoczy,J., Levine,R., Liu,G., Maclean,C., Macdonald,P., Major,J., Margulis,N., Matthews,C., McCarthy,M., McGwan,P., McKernan,K., McPherson,R., Meldrum,J., Menne,L., Mihova,T., Mlenka,V., Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Straus,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Trivis,N., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (26-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA		
REFERENCE	3 (bases 1 to 101777)		
AUTHORS	Birtten,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,S., Arachchi,H.M., Barra,N., Bairsten,V., Bloom,T., Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J.Y., Choepe,Y., Collymore,A., Cook,A., Cooke,P., Cornu,B., Dearellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., Fitzgeraid,M., Gage,D., Galagan,J., Gardyna,S., Gralham,L., Grand-Pierre,N., Hatz,N., Hagopian,D., Hagos,B., Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kelle,C., Landers,T., Levine,R., Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrum,J., Menne,L., Mihova,T., Mlenka,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., P., Ramanuja,A., Ramsamy,U., Raymond,C., Retta,R., Rise,C., Rogov,P., Roman,J., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M., Talamas,J., Testaye,S., Theodore,J., Topham,K., Travers,M., Trivis,N., Triggillo,J., Viel,R., Vo,A., Wilson,B., Wu,X., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,		

TITLE
JOURNAL
REFERENCE
AUTHORS
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (06-FEB-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 4 (bases 1 to 101777)
 Barren, B., Nusbaum, C., Lander, E., Abouelell, A., Allen, N.,
 Anderson, S., Arachchi, H.M., Barn, N., Bastien, V., Bloom, T.,
 Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y.,
 Collamore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K.,
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
 Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,
 Graham, L., Grand-Pierre, N., Hafer, N., Hagopian, D., Hago, B.,
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 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
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 Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 27, 2003 this sequence version replaced gl:2821622.
 All repeats were identified using RepeatMasker:
 Smit, A.P.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIRB
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L23062
 Center clone name: 118_p_12

 Only the middle 101.8 kilobases of this clone are being submitted.
 The remainder overlaps either accession number AC067930 [WIGCR
 project L10100]
 or accession number AC105219 [WIGCR project L23081].
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ORGANISM	REFERENCE	TITLE	JOURNAL	AUTHORS
Homo sapiens	Bakayote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	1 (bases 1 to 174906)	1 (bases 1 to 174906)	1 (bases 1 to 174906)
Homo sapiens chromosome 8, clone RP11-661A12	Unpublished	2 (bases 1 to 174906)	2 (bases 1 to 174906)	2 (bases 1 to 174906)
Birren, B., Linton, L., Nuebaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karataas, A., Klein, J., Lacombe, K., Lamazara, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Liu, G., Locke, K., MacDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrim, J., Menus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.	Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	3 (bases 1 to 174906)	3 (bases 1 to 174906)	3 (bases 1 to 174906)
Birren, B., Linton, L., Nuebaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karataas, A., Kelle, C., Lacombe, K., Lamazara, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhng, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Riebeck, M., Riley, R., Riese, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauses, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vasilleev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	Submitted (21-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	4 (bases 1 to 174906)	4 (bases 1 to 174906)	4 (bases 1 to 174906)
Birren, B., Nuebaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gind, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karataas, A., Klein, J., Lacombe, K., Lamazara, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Liu, G., Locke, K., MacDonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrim, J., Menus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.	Submitted (21-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	4 (bases 1 to 174906)	4 (bases 1 to 174906)	4 (bases 1 to 174906)

REFERENCE	TITLE	JOURNAL	AUTHORS	COMMENT
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasilev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	Submitted (24-JUL-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA	On Jul 24, 2002 this sequence version replaced gi:21490265.	All repeats were identified using RepeatMasker:	http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research	Center code: MIBR	Web site: http://www-seq.wi.mit.edu	Contact: sequence_submissions@genome.wi.mit.edu	Project Information
Center project name: L10100	Center clone name: 661_A_12			
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Best Local Similarity 100.0%; Pred. No. 1.1e-244;

Matches 907; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CCTAGGGGCTGGATTGTGTGTAAACAAGTAACTGAGGGCAGAACCCCTAGGGGA 120
DB 126354 CCTAGGGGCTGGATTGTGTGTAAACAAGTAACTGAGGGCAGAACCCCTAGGGGA 126295
QY 121 ATGCTACTCTCTCCCTTCCACTGCGCTGGTTCACGGTGGCTGGTCCCTCTTGGC 180
DB 126294 ATGCTACTCTCTCCCTTCCACTGCGCTGGTTCACGGTGGCTGGTCCCTCTTGGC 126235
QY 181 GAGAGAGTGTCTGGGTCAAGGAGCGAGAGACGCTTCAAGACTCCAGCCCTTGTATAC 240
DB 126234 GAGAGAGTGTCTGGGTCAAGGAGCGAGAGACGCTTCAAGACTCCAGCCCTTGTATAC 126175
QY 241 GAGAGAGCACTTGGCAGAGTCCAGATGGTTCGGAGTCCACACAGACTGGCGGCAAG 300
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QY 361 GGGTGGGGGGCGGCAAACTTCATAAAGAACAGAGGGTCTGGGCCCGGCACAGAGTCA 420
DB 126054 GGGTGGGGGGCGGCAAACTTCATAAAGAACAGAGGGTCTGGGCCCGGCACAGAGTCA 125995
QY 421 TCTGGCCAGCTCTCTGCTGCTGGCCAGTGGGAGTGGGACAGAGTGGGGCTTGTGCCAG 480
DB 125994 TCTGGCCAGCTCTCTGCTGCTGGCCAGTGGGAGTGGGACAGAGTGGGGCTTGTGCCAG 125935
QY 481 TAAACCAAGCTGATTTGCTGCGGGCCATGTGCTCTGCTAGGGAGCAATTTCTCA 540
DB 125934 TAAACCAAGCTGATTTGCTGCGGGCCATGTGCTCTGCTAGGGAGCAATTTCTCA 125875
QY 541 ACCTTCTGCTCTCAGAGACCCCAAGAGCTTTCATTTGATCTATTTATTTTACACATT 600
DB 125874 ACCTTCTGCTCTCAGAGACCCCAAGAGCTTTCATTTGATCTATTTATTTTACACATT 125815
QY 601 AGCAATTAACCTGAAGAAATGGGCGGGGACGGTGGCTCAGCGCTGTATCCAGACATT 660
DB 125814 AGCAATTAACCTGAAGAAATGGGCGGGGACGGTGGCTCAGCGCTGTATCCAGACATT 125755
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DB 125754 TGGAGAGCCGAGGCGGGTGAATCAGCTGAGATCAGAGATTCAAGACCACTGGCCAAACA 125695
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DB 125634 TAGTCCAGTTACTCGGAGGCTGAGGAGGAGAAATCGCTTGAACCCAGAGGCGGACGT 125575
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RESULT 8
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ACCESSION AC019122
VERSION AC019122.3 GI:8318560
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE
AUTHORS Waterston,R.H.
TITLE The sequence of Homo sapiens clone
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 207636)
TITLES Waterston,R.H.
JOURNAL Direct Submission
SUBMITTED (30-DEC-1999) Genome Sequencing Center, Washington
UNIVERSITY School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
COMMENT On Jun 7, 2000 this sequence version replaced gi:7109639.

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>

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----- Project Information -----
Center project name: H_NH0545C16
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Sequencing vector: M13; 88x
Chemistry: Dye-terminator Big Dye; 12x of reads
Assembly program: Phrap; version 0.99019
Consensus quality: 198432 bases at least Q40
Consensus quality: 201424 bases at least Q30
Consensus quality: 203070 bases at least Q20
Insert size: 18200; agarose-fp
Insert size: 206336; sum-of-coverage
Quality coverage: 6.36 in Q20 bases; sum-of-coverage
Quality coverage: 5.66 in Q20 bases; sum-of-coverage
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of 'N', but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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IN PROGRESS ***
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VERSION   AC087823.2
KEYWORDS  HTG; HTGS PHASE1.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS  Birren,B., Linton,L., Nussbaum,C. and Lander,E.
TITLE     1 (bases 1 to 164959)
JOURNAL   Homo sapiens chromosome 8, clone RP11-545C16
REFERENCE
AUTHORS  2 (bases 1 to 164959)
TITLE     Birren,B., Linton,L., Nussbaum,C. and Lander,E.
JOURNAL   Unpublished
AUTHORS  2 (bases 1 to 164959)
TITLE     Birren,B., Linton,L., Nussbaum,C., Lander,E., Allen,N., Anderson,S.,
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Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
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Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Vtel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.
COMMENT  Submitted (28-JAN-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 16, 2001 this sequence version replaced gi:12584321.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information
Center project name: L11736
Center clone name: 545_C16
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 70 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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*	82464	84226:	contig of 1763 bp in length
*	84227	84326:	gap of 100 bp
*	84327	87431:	contig of 3105 bp in length
*	87432	87531:	gap of 100 bp
*	87532	90276:	contig of 2745 bp in length
*	90277	90376:	gap of 100 bp
*	90377	93023:	contig of 2647 bp in length
*	93024	93123:	gap of 100 bp
*	93124	95831:	contig of 2708 bp in length
*	95832	95931:	gap of 100 bp
*	95832	99011:	contig of 3080 bp in length
*	99012	99111:	gap of 100 bp
*	99112	101722:	contig of 2611 bp in length
*	101723	101822:	gap of 100 bp
*	101823	105034:	contig of 3212 bp in length
*	105035	105134:	gap of 100 bp
*	105135	108113:	contig of 2979 bp in length
*	108214	108213:	gap of 100 bp
*	112105	112105:	contig of 3892 bp in length
*	112106	112205:	gap of 100 bp
*	112206	115406:	contig of 3201 bp in length
*	115407	115506:	gap of 100 bp
*	115507	119714:	contig of 4208 bp in length
*	119715	119814:	gap of 100 bp
*	119815	125158:	contig of 5344 bp in length
*	125159	125258:	gap of 100 bp
*	125259	130255:	contig of 4997 bp in length
*	130256	130355:	gap of 100 bp
*	130356	135663:	contig of 5308 bp in length
*	135664	135763:	gap of 100 bp
*	135764	141345:	contig of 5582 bp in length
*	141346	141445:	gap of 100 bp
*	14146	146381:	contig of 4936 bp in length
*	146382	146481:	gap of 100 bp
*	146482	155041:	contig of 8560 bp in length
*	155042	155141:	gap of 100 bp
*	155142	164370:	contig of 9228 bp in length
*	164371	164470:	gap of 100 bp
*	164471	164959:	contig of 489 bp in length.
Location/Qualifiers			

OY	129	TTCCTGCCCTTCCACACCTGGCCCTGGAGTTCAAGGGTGGCCCTGGTCCCTCTTSCCGAGAGAGT	188
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OY	189	GTCTCTGGGTCAAGGACCGCAGAGGACGCTCAACAATCCACAGCCCTTGTGTTACCGAGAGAC	248
Db	41562	GTCTCTGGGTCAAGGACCGCAGAGGACGCTCAACAATCCACAGCCCTTGTGTTACCGAGAGAGC	4150
OY	249	ACTTGGCAAGGTCCAGCAGATGTGTCCGAGTTCACACACAGACTGGCCGACAGGTCAGAGG	308
Db	41502	ACTTGGCAAGGTCCAGCAGATGTGTCCGAGTTCACACACAGACTGGCCGACAGGTCAGAGG	4144
OY	309	GGGACACTTCTGTGTGTGCTTGGTGTGACACATTAAGAGGGTCTTGGCCAGTCCAGGGTGGG	368
Db	41442	GGGACACTTCTGTGTGTGCTTGGTGTGACACATTAAGAGGGTCTTGGCCAGTCCAGGGTGGG	4138
OY	369	GGCGGCAAACTCCATAAAGAACAGAGGGTCTGGGCCCGCGCCACAGAGTCAATCTGCCA	428
Db	41382	GGCGGCAAACTCCATAAAGAACAGAGGGTCTGGGCCCGCGCCACAGAGTCAATCTGCCA	4132
OY	429	GCTCCTCTGCTGCTGSCCAAGTGGAGTGGCACAGAGTGGGGCTTTGTGCGCAGTAAACCA	488
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OY	489	CAGGCTGGATTGTGCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACTCTT	548
Db	41262	CAGGCTGGATTGTGCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACTCTT	4120
OY	549	GCTCTCAGGACCCCAAGAGGCTTTCATTTGATCTATTGATTTTTCACCATTAAGCAATTA	608
Db	41202	GCTCTCAGGACCCCAAGAGGCTTTCATTTGATCTATTGATTTTTCACCATTAAGCAATTA	4114
OY	609	AAACTGAGAAATGGGCCCGGGCACGGTGGCTCACGCTGTATATCCACACCTTTGGGAGGC	668
Db	41142	AAACTGAGAAATGGGCCCGGGCACGGTGGCTCACGCTGTATATCCACACCTTTGGGAGGC	4108
OY	669	CGAGGCGGGTGGATCACTGAGATCAGAGGTTCAAGACACAGCCCTGGCCCAATGTTGAA	728
Db	41082	CGAGGCGGGTGGATCACTGAGATCAGAGGTTCAAGACACAGCCCTGGCCCAATGTTGAA	4102
OY	729	CCTTGTCTACTAAATAATACAAAATTTAGCCAGGCAAGTGTGTGCACTGTGATGCCA	788
Db	41022	CCTTGTCTACTAAATAATACAAAATTTAGCCAGGCAAGTGTGTGCACTGTGATGCCA	4096
OY	789	GTTACTCGGGAGGCTGAGGCGAGAAAATCGTTTGAATCCACAGAGCGGACGTTGCGGTGA	848
Db	40962	GTTACTCGGGAGGCTGAGGCGAGAAAATCGTTTGAATCCACAGAGCGGACGTTGCGGTGA	4090
OY	849	GCCGAGATCGGCGCGCTGATTTCCAGCCTCGGGCCGACAGAGTGAAGATCTCAATCTCACCA	907
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RESULT	10			
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LOCUS	ARI129215	500 bp	DNA	
DEFINITION	Sequence	73 from patent US 6183968.		
ACCESSION	ARI129215			
VERSION	ARI129215.1	GI:14116877		
KEYWORDS				
				linear
				PAT 16-MAY-2001

ORGANISM	REFERENCE	AUTHORS
Unknown.	1 (bases 1 to 500)	Hillman, J. L., Yue, H., Reddy, R., Guegler, K. J.
Unclassified.		Bandman, O., Lal, P.

TITLE	Composition for the detection of genes encoding receptors and proteins associated with cell proliferation
JOURNAL	Patent: US 6183968-A 73 06-FEB-2001;

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source      Location/Qualifiers
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Db 245 CTTCGACAGTCAGGGGTGGGGGGGCGCAATCCATTAAGAACAGAGGCTT-GGCCCC 187
Qy 408 GGCACAGAGTCATCTGCCCCAGCTCTCTGTGTGCGCAAGTGGAGTGGCAGAGTGG 467
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Db 126 GGCCTTGTGCGCAATTAAGCAAGAGCTGTGATTTG-CTGCGGGCCATGCTCTGTAAG 68
Qy 528 GCAGCAATTCACCTTCTGTGCTCTGAGACCCCAAGAGCTTCATTTATCTATTGA 587
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DEFINITION Sequence 3599 from Patent WO0192581.
ACCESSION CQ460821
VERSION CQ460821.1 GI:41426440
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
Algate,P.A., Harlocker,S.L. and Jones,R.
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Compositions and methods for the therapy and diagnosis of
ovariencancer
Patent: WO 0192581-A 3599 06-DEC-2001;
JOURNAL CORIXA CORPORATION (US)
FEATURES
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Location/Qualifiers
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Qy 310 GACAGTTCGTGTGTGCTGTGTGAGCAGTAAGAGGTCTTGGCCAGTCAAGGTTGGGG 369
Db 282 GACAGTTCGTGTGTGCTGTGTGAGCAGTAAGAGGTCTTGGCCAGTCAAGGTTGGGG 223
Qy 370 GCGGCAATCTCATTAAGAACAGAGGCTTGGGGCCCGGCAAGAGTCAATTCGCCAG 429
Db 222 GCGGCAATCTCATTAAGAACAGAGGCTT-GGCCCCGCGCAAGAGTCAATTCGCCAG 164
Qy 430 CTCCTGTGCTGTGGCCAGTGGAGTGGCAGAGGTTGGGCTTTGTGTGCAATAAACAC 489
Db 163 CTCCTGTGCTGTGGCCAGTGGAGTGGCAGAGGTTGGGCTTTGTGTGCAATAAACAC 104
Qy 490 AGGCTGATTTGCTGTGCGGCGCATGTGTCCTGTCTAGGGCAGCAATTCCTCAACTTTG 549

Db 103 AGGCTGATTTG-CTGCGGGCCAT-CTCCCTGTCTAGGGCAGCAATTCCTCAACTTTG 46
Qy 550 CTCTCAGAACCCCAAGAGCTTCATTTATCTATTGATTTTAC 594
Db 45 CTCTCAGAACCCCAAGAGCTTCATTTATCTATTGATTTTAC 1

RESULT 14
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DEFINITION Sequence 6113 from Patent WO0192581.
ACCESSION CQ463335
VERSION CQ463335.1 GI:41428954
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
Algate,P.A., Harlocker,S.L. and Jones,R.
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Compositions and methods for the therapy and diagnosis of
ovariencancer
Patent: WO 0192581-A 6113 06-DEC-2001;
JOURNAL CORIXA CORPORATION (US)
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Location/Qualifiers
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Qy 414 AGAGTCATCTGCCAGTCTCTGTGCTGTGCGGCGGAGTGGAGCAGAGTGGGGCTT 473
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Qy 474 GTGCAAGTAAGAACAGAGGCTGTGCTGTGCGGCGGCGGAGTGGGGCTTCTAGGGCAGCA 533
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Qy 594 C 594
Db 1 C 1

RESULT 15
LOCUS AX071596 399 bp DNA linear PAT 25-JAN-2001
DEFINITION Sequence 2068 from Patent WO0102568.
ACCESSION AX071596
VERSION AX071596.1 GI:12581947
KEYWORDS
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS Williams,L.T., Escobedo,J., Inliss,M.A., Garcia,P.D., Klinger,J.,
Kassam,A., Reinhard,C., Randazzo,F., Kennedy,G.C., Pot,D.,
Lamsom,G., Drmanac,R., Crkenjakov,R., Drmanac,S., Dickson,M.,
Labat,I., Leshkowitz,D., Kita,D., Garcia,V. and Strache-Crain,B.
TITLE Human genes and gene expression products
JOURNAL Patent: WO 0102568-A 2068 11-JAN-2001;
CHIRON CORPORATION (US) ; HYSEQ, INC. (US)
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Best Local Similarity 99.1%; Pred. No. 1.2e-51;
Matches 224; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 121 ATGCTACCTCTGCTGCCCTTCCACCTGCGCTGTTCACGGTGGCTGTGTCCTCTTGCC 180
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Qy 181 GAGAGAGTGTCTGTGGTCAAGGAGCGCAGAGAGCGTCAAGACTCC 226
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GenCore version 5.1.6
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OM nucleic - nucleic search, using ew model

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179	907	100.0	907	Sequence 1596, App
180	601.6	66.3	1154	Sequence 204, App
181	458	50.3	480	Sequence 5524, App
182	403	44.4	425	Sequence 3167, App

C 183	369	40.7	402	9	US-09-867-701-3599	Sequence 3599, App
C 184	344.2	37.9	360	9	US-09-867-701-6113	Sequence 6113, App
185	213	23.5	10093	9	US-09-764-869-1390	Sequence 1390, App
186	213	23.5	10093	14	US-10-091-504-1390	Sequence 1390, App
187	213	23.5	10093	17	US-10-227-577-1390	Sequence 1390, App
188	212.8	23.5	32148	10	US-09-764-891-6906	Sequence 6906, App
189	212.2	23.4	17397	9	US-09-764-869-1945	Sequence 1945, App
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193	212.2	23.4	19334	14	US-10-091-504-1943	Sequence 1943, App
194	212.2	23.4	19334	17	US-09-764-869-1943	Sequence 1943, App
195	212.2	23.4	19345	9	US-09-764-869-1944	Sequence 1944, App
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C 199	211.8	23.4	177587	13	US-10-087-192-1438	Sequence 1438, App
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C 201	211.2	23.3	24664	9	US-09-764-867-613	Sequence 613, App
C 202	211.2	23.3	24664	14	US-10-073-961-613	Sequence 613, App
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204	210	23.2	301	15	US-10-255-434-1	Sequence 15, App
205	209.6	23.1	28316	22	US-10-893-315-165	Sequence 165, App
206	209.6	23.1	28316	22	US-10-893-315-166	Sequence 166, App
207	209.4	23.1	19616	9	US-09-764-877-3220	Sequence 3220, App
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209	209.4	23.1	124596	22	US-10-981-277-39	Sequence 39, App
210	209.4	23.1	152744	22	US-10-981-277-41	Sequence 41, App
211	209.4	23.1	153191	22	US-10-981-277-40	Sequence 40, App
212	209.4	23.1	181279	22	US-10-981-277-38	Sequence 38, App
213	209.2	23.1	614	10	US-09-764-891-9433	Sequence 9433, App
214	209.2	23.1	614	17	US-10-091-414-301	Sequence 301, App
215	209.2	23.1	614	17	US-09-764-891-9431	Sequence 9431, App
216	209.2	23.1	691	10	US-10-091-414-289	Sequence 289, App
C 217	209.2	23.1	2470	13	US-10-027-632-110237	Sequence 110237, App
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222	209.2	23.1	16225	17	US-10-091-414-300	Sequence 300, App
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C 224	209.2	23.1	59065	16	US-10-135-696-3	Sequence 3, App
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C 227	209	23.0	122673	22	US-10-737-082-33	Sequence 33, App
C 228	209	23.0	122673	22	US-10-765-790-33	Sequence 7048, App
C 229	209	23.0	330926	20	US-10-719-993-7048	Sequence 454, App
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236	208.6	23.0	518	14	US-10-092-154-1799	Sequence 1799, App
237	208.6	23.0	167163	17	US-10-394-948-31	Sequence 31, App
C 238	208.2	23.0	171843	22	US-10-981-277-44	Sequence 44, App
239	208	22.9	291	9	US-09-964-824-509	Sequence 509, App
240	208	22.9	291	9	US-09-969-347-1	Sequence 1, App
241	208	22.9	291	9	US-10-843-641A-5812	Sequence 5812, App
242	208	22.9	291	19	US-10-843-641A-6130	Sequence 8130, App
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C 248	207.6	22.9	73764	19	US-10-741-601-5616	Sequence 5616, App
C 249	207.6	22.9	93011	20	US-10-719-993-6871	Sequence 6871, App
C 250	207.2	22.8	403055	19	US-10-322-696-70	Sequence 70, App
C 251	206.8	22.8	169659	11	US-10-997-632-121880	Sequence 22, App
C 252	206.4	22.8	96594	13	US-10-027-632-151880	Sequence 191880, App
C 253	206.2	22.7	603	13	US-10-027-632-151880	Sequence 191880, App
C 254	206.2	22.7	603	17	US-10-027-632-151880	Sequence 952, App
C 255	206.2	22.7	34096	13	US-10-087-192-952	Sequence 952, App

C 256	206.2	22.7	48436	9	US-09-927-602-38	Sequence 38, Appl	C 329	204	22.5	33137	17	US-10-292-798-913	Sequence 913, App
C 257	206	22.7	113486	20	US-10-417-375-18	Sequence 18, Appl	C 330	204	22.5	48841	10	US-09-844-653-32	Sequence 32, Appl
C 258	205.8	22.7	131968	13	US-10-087-197-46	Sequence 46, Appl	C 331	204	22.5	81924	19	US-10-741-601-8636	Sequence 5636, Ap
C 259	205.8	22.7	59554	18	US-10-052-482-202	Sequence 202, App	C 332	203.8	22.5	717	13	US-10-027-632-130796	Sequence 130796,
C 260	205.8	22.7	203654	2	US-09-820-905-3	Sequence 3, Appl1	C 333	203.8	22.5	717	13	US-10-027-632-130796	Sequence 130796,
C 261	205.8	22.7	203654	22	US-10-473-338A-3	Sequence 3, Appl1	C 334	203.8	22.5	892	17	US-10-027-632-164445	Sequence 164445,
C 262	205.8	22.7	260549	21	US-10-741-600-17723	Sequence 17723, A	C 335	203.8	22.5	835	18	US-10-027-632-164445	Sequence 164445,
C 263	205.6	22.7	10085	10	US-09-764-891-5591	Sequence 5491, Ap	C 336	203.8	22.5	16540	18	US-10-344-394-13	Sequence 13, Appl
C 264	205.6	22.7	142519	22	US-10-479-877A-9	Sequence 9, Appl	C 337	203.8	22.5	8735	18	US-10-344-394-1	Sequence 1, Appl1
C 265	205.4	22.6	710	13	US-10-027-632-110510	Sequence 110510,	C 338	203.8	22.5	16540	21	US-10-741-601-17666	Sequence 17666, Ap
C 266	205.4	22.6	710	17	US-10-027-632-110510	Sequence 110510,	C 339	203.8	22.5	16540	21	US-10-741-601-17666	Sequence 17666, Ap
C 267	205.4	22.6	860	13	US-10-027-632-130797	Sequence 130797,	C 340	203.8	22.5	18335	19	US-10-741-601-5717	Sequence 17817, A
C 268	205.4	22.6	860	17	US-10-027-632-130797	Sequence 130797,	C 341	203.8	22.5	18335	21	US-10-741-600-17831	Sequence 17831, A
C 269	205.4	22.6	2619	19	US-10-363-829-250	Sequence 250, App	C 342	203.8	22.5	50461	17	US-10-052-482-220	Sequence 220, App
C 270	205.4	22.6	56516	9	US-09-901-484A-1	Sequence 1, Appl1	C 343	203.6	22.4	60461	18	US-10-341-434-82	Sequence 82, Appl
C 271	205.4	22.6	56516	9	US-09-853-526-1	Sequence 1, Appl1	C 344	203.4	22.4	888	13	US-10-027-632-121467	Sequence 121467,
C 272	205.4	22.6	56520	9	US-09-901-484A-179	Sequence 179, App	C 345	203.4	22.4	888	17	US-10-027-632-121467	Sequence 121467,
C 273	205.4	22.6	56520	9	US-09-853-526-179	Sequence 179, App	C 346	203.4	22.4	4067	10	US-09-764-891-7222	Sequence 7225, Ap
C 274	205.4	22.6	67253	22	US-10-737-082-88	Sequence 88, Appl	C 347	203.4	22.4	4067	10	US-09-764-891-7225	Sequence 338, App
C 275	205.4	22.6	67253	22	US-10-765-790-88	Sequence 88, Appl	C 348	203.4	22.4	32190	9	US-09-764-887-338	Sequence 338, App
C 276	205.4	22.6	96594	11	US-09-997-722-154	Sequence 154, App	C 349	203.4	22.4	32190	14	US-10-073-961-338	Sequence 17, Appl
C 277	205.4	22.6	150535	22	US-10-981-277-36	Sequence 36, Appl	C 350	203.4	22.4	56737	9	US-09-782-378A-17	Sequence 17, Appl
C 278	205.4	22.6	166536	22	US-10-981-277-35	Sequence 35, Appl	C 351	203.4	22.4	191395	18	US-10-235-132A-45	Sequence 45, Appl
C 279	205.2	22.6	301	15	US-10-255-434-2	Sequence 2, Appl1	C 352	203.4	22.4	238417	21	US-10-461-862-98	Sequence 98, Appl
C 280	205.2	22.6	1098	13	US-10-027-632-10720	Sequence 10720, A	C 353	203.2	22.4	194883	13	US-10-087-192-826	Sequence 826, App
C 281	205.2	22.6	1098	17	US-10-514-744-42	Sequence 10720, A	C 354	203.2	22.4	256190	19	US-10-322-281-320	Sequence 320, App
C 282	205.2	22.6	3660	22	US-10-514-744-3	Sequence 42, Appl	C 355	203	22.4	718	13	US-10-027-632-102137	Sequence 102137,
C 283	205.2	22.6	3673	22	US-10-514-744-3	Sequence 3, Appl1	C 356	203	22.4	718	13	US-10-027-632-102138	Sequence 102138,
C 284	205.2	22.6	3673	22	US-10-514-744-9	Sequence 9, Appl1	C 357	203	22.4	718	17	US-10-027-632-102138	Sequence 102138,
C 285	205.2	22.6	3674	22	US-10-514-744-1	Sequence 1, Appl1	C 358	203	22.4	718	17	US-10-027-632-102138	Sequence 102138,
C 286	205.2	22.6	3674	22	US-10-514-744-11	Sequence 11, Appl1	C 359	203	22.4	99014	9	US-09-880-107-3428	Sequence 3428, Ap
C 287	205.2	22.6	3675	22	US-10-514-744-7	Sequence 7, Appl1	C 360	203	22.4	114793	5	US-10-148-806-3	Sequence 3, Appl1
C 288	205.2	22.6	3702	22	US-10-514-744-5	Sequence 5, Appl1	C 361	203	22.4	114793	19	US-10-859-792-3	Sequence 3, Appl1
C 289	205.2	22.6	14558	21	US-10-741-600-15669	Sequence 15669, A	C 362	203	22.4	193074	22	US-10-981-277-43	Sequence 43, Appl
C 290	205.2	22.6	17138	21	US-10-741-600-18009	Sequence 18009, A	C 363	203	22.4	193074	22	US-10-981-277-43	Sequence 43, Appl
C 291	205.2	22.6	18303	17	US-10-741-600-17807	Sequence 17807, A	C 364	203	22.4	1790242	20	US-10-719-993-6940	Sequence 6940, Ap
C 292	205.2	22.6	51001	21	US-10-189-268-11	Sequence 11, Appl	C 365	202.8	22.4	3753	10	US-09-764-891-7624	Sequence 7624, Ap
C 293	205	22.6	227968	14	US-10-723-860-1357	Sequence 1357, Ap	C 366	202.8	22.4	14448	9	US-09-860-670-250	Sequence 250, App
C 294	204.8	22.6	289	20	US-10-115-278-3	Sequence 3, Appl1	C 367	202.8	22.4	14448	17	US-10-227-646-250	Sequence 253, App
C 295	204.8	22.6	289	20	US-10-762-966-3	Sequence 3, Appl1	C 368	202.8	22.4	14451	17	US-09-860-670-253	Sequence 253, App
C 296	204.8	22.6	51001	17	US-10-189-268-11	Sequence 11, Appl	C 369	202.8	22.4	14451	17	US-10-227-646-253	Sequence 253, App
C 297	204.8	22.6	108316	17	US-10-292-798-1789	Sequence 1789, Ap	C 370	202.8	22.4	22259	10	US-09-764-881-6605	Sequence 6605, Ap
C 298	204.8	22.6	108317	15	US-10-017-161-2143	Sequence 2143, Ap	C 371	202.8	22.4	22699	14	US-10-091-572-169	Sequence 469, App
C 299	204.8	22.6	168749	17	US-10-085-117-250	Sequence 250, App	C 372	202.8	22.4	27067	10	US-09-841-158-5	Sequence 5, Appl1
C 300	204.8	22.6	684973	9	US-09-263-959-1	Sequence 1, Appl1	C 373	202.8	22.4	27067	19	US-10-801-837-5	Sequence 5, Appl1
C 301	204.6	22.6	96589	13	US-10-085-117-130	Sequence 130, App	C 374	202.8	22.4	99886	13	US-10-087-192-328	Sequence 328, App
C 302	204.6	22.6	122614	17	US-10-087-192-1726	Sequence 1726, Ap	C 375	202.8	22.4	101885	20	US-10-723-860-146	Sequence 146, App
C 303	204.6	22.6	247682	18	US-10-235-192A-28	Sequence 28, Appl	C 376	202.8	22.4	133532	13	US-10-087-192-1810	Sequence 1810, Ap
C 304	204.4	22.5	14417	9	US-09-860-670-251	Sequence 251, App	C 377	202.6	22.3	702	13	US-10-027-632-136699	Sequence 136699,
C 305	204.4	22.5	14426	17	US-10-227-646-251	Sequence 251, App	C 378	202.6	22.3	702	17	US-10-027-632-136699	Sequence 136699,
C 306	204.4	22.5	14426	17	US-09-860-670-249	Sequence 249, App	C 379	202.6	22.3	3353	9	US-09-963-159-1	Sequence 1, Appl1
C 307	204.4	22.5	14426	17	US-10-227-646-249	Sequence 249, App	C 380	202.6	22.3	3353	18	US-10-423-543-43	Sequence 43, Appl
C 308	204.4	22.5	20538	21	US-10-741-600-17954	Sequence 17954, A	C 381	202.6	22.3	3360	17	US-10-311-034-38	Sequence 38, Appl
C 309	204.4	22.5	23597	21	US-10-741-600-17628	Sequence 17628, A	C 382	202.6	22.3	3343	20	US-10-370-715B-639	Sequence 639, App
C 310	204.4	22.5	167163	17	US-10-394-948-31	Sequence 31, Appl	C 383	202.6	22.3	20669	6	US-09-764-886-2427	Sequence 2427, Ap
C 311	204.4	22.5	4736	17	US-10-452-510-15	Sequence 15, Appl	C 384	202.6	22.3	20669	14	US-10-091-504-4247	Sequence 4247, Ap
C 312	204.2	22.5	4736	18	US-10-617-334-15	Sequence 15, Appl	C 385	202.6	22.3	20669	17	US-10-227-577-2427	Sequence 2427, Ap
C 313	204.2	22.5	4736	19	US-10-744-465-15	Sequence 15, Appl	C 386	202.4	22.3	585	13	US-10-027-632-273703	Sequence 273703,
C 314	204.2	22.5	4736	19	US-10-833-679-15	Sequence 15, Appl	C 387	202.4	22.3	585	17	US-10-027-632-273703	Sequence 273703,
C 315	204.2	22.5	4736	22	US-10-818-279-15	Sequence 15, Appl	C 388	202.4	22.3	795	13	US-10-027-632-171351	Sequence 171351,
C 316	204.2	22.5	11754	10	US-09-984-827-5	Sequence 5, Appl1	C 389	202.4	22.3	795	17	US-10-027-632-171351	Sequence 171351,
C 317	204.2	22.5	83712	19	US-10-741-601-5705	Sequence 5705, Ap	C 390	202.4	22.3	32195	9	US-09-764-870-617	Sequence 617, App
C 318	204.2	22.5	83712	21	US-10-741-600-17805	Sequence 17805, A	C 391	202.4	22.3	32195	9	US-09-764-870-617	Sequence 617, App
C 319	204.2	22.5	155572	22	US-10-981-277-30	Sequence 30, Appl	C 392	202.4	22.3	32195	9	US-09-764-886-1605	Sequence 1605, Ap
C 320	204.2	22.5	159138	20	US-10-719-993-6777	Sequence 6777, Ap	C 393	202.4	22.3	32195	11	US-09-764-886-1605	Sequence 1611, App
C 321	204.2	22.5	159138	21	US-10-741-600-17613	Sequence 17613, A	C 394	202.4	22.3	32195	14	US-10-125-540-611	Sequence 617, App
C 322	204.2	22.5	183999	19	US-10-745-377-1	Sequence 1, Appl1	C 395	202.4	22.3	32195	14	US-10-125-540-611	Sequence 1605, Ap
C 323	204.2	22.5	183999	20	US-10-872-113-1	Sequence 1, Appl1	C 396	202.4	22.3	32195	17	US-10-091-504-1505	Sequence 1505, Ap
C 324	204	22.5	691	13	US-10-027-632-263957	Sequence 263957,	C 397	202.4	22.3	32195	17	US-10-227-577-1505	Sequence 1505, Ap
C 325	204	22.5	691	13	US-10-027-632-263957	Sequence 263957,	C 398	202.4	22.3	43712	20	US-10-723-860-15765	Sequence 1576, Ap
C 326	204	22.5	820	17	US-10-027-632-25801	Sequence 25801, A	C 399	202.4	22.3	59942	19	US-10-741-601-5775	Sequence 5775, Ap
C 327	204	22.5	820	17	US-10-027-632-25801	Sequence 25801, A	C 400	202.4	22.3	129381	21	US-10-461-862-28	Sequence 28, Appl
C 328	204	22.5	22927	10	US-09-764-891-7470	Sequence 7470, Ap	C 401	202.2	22.3	850	13	US-10-027-632-30982	Sequence 30982, A

C 402	202.2	22.3	850	17	US-10-027-632-30982	Sequence 30982, A	C 475	201.6	22.2	8896	17	US-10-074-024-666	Sequence 666, App
C 403	202.2	22.3	1158	13	US-10-027-632-122621	Sequence 122621	C 476	201.6	22.2	12430	16	US-10-300-453A-26	Sequence 26, App
C 404	202.2	22.3	1158	13	US-10-027-632-122622	Sequence 122622	C 477	201.6	22.2	14405	16	US-10-300-453A-27	Sequence 27, App
C 405	202.2	22.3	1158	13	US-10-027-632-122623	Sequence 122623	C 478	201.6	22.2	17158	17	US-10-264-237-2833	Sequence 2833, App
C 406	202.2	22.3	1158	17	US-10-027-632-122621	Sequence 122621	C 479	201.6	22.2	32134	17	US-10-242-355-936	Sequence 936, App
C 407	202.2	22.3	1158	17	US-10-027-632-122622	Sequence 122622	C 480	201.6	22.2	32192	17	US-10-242-355-937	Sequence 937, App
C 408	202.2	22.3	1158	17	US-10-027-632-122623	Sequence 122623	C 481	201.6	22.2	50602	13	US-10-087-192-448	Sequence 448, App
C 409	202.2	22.3	1369	13	US-10-027-632-124038	Sequence 124038	C 482	201.6	22.2	73764	19	US-10-741-601-5616	Sequence 5616, App
C 410	202.2	22.3	1369	13	US-10-027-632-124039	Sequence 124039	C 483	201.6	22.2	235039	15	US-10-301-844-2	Sequence 1, App
C 411	202.2	22.3	1369	13	US-10-027-632-124040	Sequence 124040	C 484	201.6	22.2	237326	15	US-10-301-844-1	Sequence 2, App
C 412	202.2	22.3	1369	17	US-10-027-632-124038	Sequence 124038	C 485	201.4	22.2	406	10	US-09-918-995-8791	Sequence 8791, App
C 413	202.2	22.3	1369	17	US-10-027-632-124039	Sequence 124039	C 486	201.4	22.2	11722	10	US-09-855-612-1	Sequence 1, App
C 414	202.2	22.3	1369	17	US-10-027-632-124040	Sequence 124040	C 487	201.4	22.2	15783	10	US-09-764-872-700	Sequence 700, App
C 415	202.2	22.3	1369	17	US-10-027-632-124038	Sequence 124038	C 488	201.4	22.2	28953	20	US-10-719-993-6811	Sequence 6811, App
C 416	202.2	22.3	1369	17	US-10-027-632-124039	Sequence 124039	C 489	201.4	22.2	29283	19	US-10-741-601-5720	Sequence 5720, App
C 417	202.2	22.3	1369	17	US-10-027-632-124040	Sequence 124040	C 490	201.4	22.2	42954	13	US-10-087-192-934	Sequence 934, App
C 418	202.2	22.3	1369	16	US-10-286-926-8	Sequence 8	C 491	201.4	22.2	59856	13	US-10-087-192-664	Sequence 664, App
C 419	202.2	22.3	1369	16	US-10-286-926-8	Sequence 8	C 492	201.4	22.2	64467	14	US-10-374-409-3	Sequence 3, App
C 420	202.2	22.3	1369	16	US-10-286-926-8	Sequence 8	C 493	201.4	22.2	64467	21	US-10-932-135-3	Sequence 3, App
C 421	202.2	22.3	1369	16	US-10-286-926-8	Sequence 8	C 494	201.4	22.2	64467	21	US-10-932-135-3	Sequence 3, App
C 422	202.2	22.3	1369	16	US-10-286-926-8	Sequence 8	C 495	201.4	22.2	64467	21	US-10-932-135-3	Sequence 3, App
C 423	202.2	22.3	1369	16	US-10-286-926-8	Sequence 8	C 496	201.4	22.2	64467	21	US-10-932-135-3	Sequence 3, App
C 424	202.2	22.3	1369	16	US-10-286-926-8	Sequence 8	C 497	201.4	22.2	64467	21	US-10-932-135-3	Sequence 3, App
C 425	202.2	22.3	1369	16	US-10-286-926-8	Sequence 8	C 498	201.4	22.2	64467	21	US-10-932-135-3	Sequence 3, App
C 426	202.2	22.3	1369	16	US-10-286-926-8	Sequence 8	C 499	201.4	22.2	64467	21	US-10-932-135-3	Sequence 3, App
C 427	202.2	22.3	1369	16	US-10-286-926-8	Sequence 8	C 500	201.4	22.2	64467	21	US-10-932-135-3	Sequence 3, App

548	200.8	22.1	679	17	US-10-027-633-102522	Sequence 102522,	621	200.2	22.1	125534	13	US-10-087-192-1678	Sequence 1678, Ap
549	200.8	22.1	679	17	US-10-027-633-102523	Sequence 102523,	622	200.2	22.1	143973	12	US-10-087-192-442	Sequence 442, Ap
550	200.8	22.1	679	17	US-10-027-633-102524	Sequence 102524,	623	200.2	22.1	150275	13	US-10-081-277-55	Sequence 55, Appl
551	200.8	22.1	696	13	US-10-027-633-212772	Sequence 212772,	624	200.2	22.1	174566	14	US-10-020-111-1	Sequence 1, Appl
552	200.8	22.1	696	13	US-10-027-633-212772	Sequence 212772,	625	200.2	22.1	174566	13	US-10-235-192A-37	Sequence 37, Appl
553	200.8	22.1	4421	14	US-10-216-337-6	Sequence 6, Appl	626	200.2	22.1	256157	18	US-10-087-192-1204	Sequence 1204, Ap
554	200.8	22.1	17263	19	US-10-741-601-5722	Sequence 5722, Ap	627	200.2	22.1	256157	13	US-10-322-281-776	Sequence 776, Ap
555	200.8	22.1	17263	19	US-10-741-600-17846	Sequence 17846, A	628	200	22.1	626	13	US-10-027-632-133310	Sequence 133310,
556	200.8	22.1	22645	10	US-09-764-891-7673	Sequence 7673, Ap	629	200	22.1	626	17	US-10-027-632-133310	Sequence 133310,
557	200.8	22.1	22645	10	US-09-764-891-8183	Sequence 8183, Ap	630	200	22.1	1061	16	US-10-277-161-66	Sequence 66, Appl
558	200.8	22.1	66916	19	US-10-741-601-5708	Sequence 5708, Ap	631	200	22.1	1994	13	US-10-027-632-262627	Sequence 262627,
559	200.8	22.1	66916	21	US-10-741-600-17810	Sequence 17810, A	632	200	22.1	1994	13	US-10-027-632-262628	Sequence 262628,
560	200.8	22.1	96593	18	US-10-052-482-106	Sequence 106, App	633	200	22.1	1994	13	US-10-027-632-262629	Sequence 262629,
561	200.8	22.1	107820	19	US-09-792-616-1	Sequence 1, Appl	634	200	22.1	1994	17	US-10-027-632-262628	Sequence 262628,
562	200.8	22.1	107820	19	US-10-764-328-1	Sequence 56, Appl	635	200	22.1	1994	17	US-10-027-632-262628	Sequence 262628,
563	200.8	22.1	15053	22	US-10-981-277-56	Sequence 56, Appl	636	200	22.1	1994	17	US-10-027-632-262629	Sequence 262629,
564	200.8	22.1	172984	21	US-10-484-577-661	Sequence 856, App	637	200	22.1	2240	13	US-10-027-632-103336	Sequence 103336,
565	200.8	22.1	213040	13	US-10-087-192-856	Sequence 856, App	638	200	22.1	2240	17	US-10-027-632-103336	Sequence 103336,
566	200.8	22.1	319608	17	US-10-147-603-1	GENERAL INFORMAT	639	200	22.1	8895	9	US-09-764-855-332	Sequence 332, App
567	200.6	22.1	5668	17	US-10-074-024-751	Sequence 751, App	640	200	22.1	8895	14	US-10-072-349-332	Sequence 332, App
568	200.6	22.1	8894	9	US-09-764-847-1606	Sequence 1606, Ap	641	200	22.1	8895	17	US-10-074-024-668	Sequence 668, App
569	200.6	22.1	8894	14	US-10-092-154-1606	Sequence 1606, Ap	642	200	22.1	36110	19	US-10-741-601-5675	Sequence 5675, Ap
570	200.6	22.1	26393	15	US-10-017-161-1653	Sequence 1653, Ap	643	200	22.1	36110	20	US-10-719-993-8850	Sequence 8850, Ap
571	200.6	22.1	48680	13	US-10-087-192-2044	Sequence 2044, Ap	644	200	22.1	46649	22	US-09-805-456-3	Sequence 3, Appl
572	200.6	22.1	49736	20	US-10-719-993-7050	Sequence 7050, Ap	645	200	22.1	46649	22	US-10-679-362-3	Sequence 3, Appl
573	200.6	22.1	55827	9	US-09-813-133A-3	Sequence 3, Appl	646	200	22.1	47196	21	US-10-741-600-17636	Sequence 17636, A
574	200.6	22.1	55827	14	US-10-212-877-3	Sequence 3, Appl	647	200	22.1	50000	17	US-10-364-505-7	Sequence 7, Appl
575	200.6	22.1	55827	21	US-10-954-110-3	Sequence 3, Appl	648	200	22.1	50000	19	US-10-681-199-7	Sequence 7, Appl
576	200.6	22.1	96595	17	US-10-034-650-34	Sequence 34, Appl	649	200	22.1	60330	13	US-10-087-192-1732	Sequence 1732, Ap
577	200.6	22.1	106344	10	US-09-910-185-10	Sequence 10, Appl	650	200	22.1	77992	16	US-10-225-810-11	Sequence 11, Appl
578	200.6	22.1	172569	13	US-10-087-192-1366	Sequence 1366, Ap	651	200	22.1	109906	18	US-10-235-192A-31	Sequence 31, Appl
579	200.6	22.1	172570	19	US-10-450-826-114	Sequence 114, App	652	200	22.1	161334	13	US-10-087-192-7130	Sequence 730, App
580	200.6	22.1	173308	22	US-10-756-149-639	Sequence 629, App	653	200	22.1	208700	18	US-10-388-838-4	Sequence 4, Appl
581	200.6	22.1	246144	13	US-10-085-117-226	Sequence 226, App	654	200	22.1	304905	16	US-10-271-416-1	Sequence 1, Appl
582	200.6	22.1	260027	17	US-10-087-192-298	Sequence 298, App	655	200	22.1	401433	22	US-10-737-082-19	Sequence 79, Appl
583	200.4	22.1	13278	18	US-10-712-363-5	Sequence 5, Appl	656	200	22.1	401433	21	US-10-765-790-79	Sequence 4, Appl
584	200.4	22.1	13677	18	US-10-712-363-6	Sequence 6, Appl	657	200	22.1	653350	22	US-10-461-862-4	Sequence 2, Appl
585	200.4	22.1	14317	20	US-10-808-522-3	Sequence 3, Appl	658	199.8	22.0	465	19	US-10-674-124A-23132	Sequence 23132, A
586	200.4	22.1	21936	10	US-09-764-891-8807	Sequence 8807, Ap	659	199.8	22.0	560	13	US-10-027-632-276693	Sequence 276693,
587	200.4	22.1	21936	10	US-09-764-891-9446	Sequence 9446, Ap	660	199.8	22.0	560	17	US-10-027-632-276893	Sequence 276893,
588	200.4	22.1	21936	17	US-10-091-414-314	Sequence 314, App	661	199.8	22.0	614	13	US-10-027-632-287641	Sequence 287641,
589	200.4	22.1	26657	16	US-10-395-242-3	Sequence 3, Appl	662	199.8	22.0	614	17	US-10-027-632-287641	Sequence 287641,
590	200.4	22.1	30753	22	US-10-737-082-24	Sequence 24, Appl	663	199.8	22.0	738	13	US-10-027-632-27194	Sequence 27193, A
591	200.4	22.1	30753	22	US-10-765-790-24	Sequence 24, Appl	664	199.8	22.0	738	13	US-10-027-632-27194	Sequence 27193, A
592	200.4	22.1	102790	21	US-10-367-094-153	Sequence 153, App	665	199.8	22.0	738	17	US-10-027-632-27194	Sequence 27193, A
593	200.4	22.1	102790	21	US-10-741-600-17809	Sequence 17809, A	666	199.8	22.0	738	17	US-10-027-632-27194	Sequence 27193, A
594	200.4	22.1	109730	21	US-10-741-600-17809	Sequence 17809, A	667	199.8	22.0	2131	13	US-10-027-632-28353	Sequence 28353, A
595	200.4	22.1	142201	20	US-10-719-993-6669	Sequence 6669, App	668	199.8	22.0	2131	13	US-10-027-632-103101	Sequence 103101,
596	200.4	22.1	161051	20	US-10-417-375-170	Sequence 170, App	669	199.8	22.0	2131	13	US-10-027-632-103101	Sequence 103101,
597	200.4	22.1	175077	13	US-10-087-192-1168	Sequence 1168, Ap	670	199.8	22.0	2131	17	US-10-027-632-28353	Sequence 28353, A
598	200.4	22.1	183046	22	US-10-981-227-31	Sequence 31, Appl	671	199.8	22.0	2131	17	US-10-027-632-103101	Sequence 103101,
599	200.4	22.1	227968	20	US-10-723-860-1357	Sequence 1357, Ap	672	199.8	22.0	2131	17	US-10-027-632-103102	Sequence 103102,
600	200.2	22.1	283	22	US-10-984-180-1	Sequence 1, Appl	673	199.8	22.0	2306	9	US-09-764-877-3604	Sequence 3604, Ap
601	200.2	22.1	601	19	US-10-834-850-18	Sequence 18, Appl	674	199.8	22.0	2306	17	US-10-242-515-5604	Sequence 5604, Ap
602	200.2	22.1	650	13	US-10-027-632-197409	Sequence 197409,	675	199.8	22.0	2311	9	US-09-764-877-3605	Sequence 3605, Ap
603	200.2	22.1	650	13	US-10-027-632-197410	Sequence 197410,	676	199.8	22.0	2311	17	US-10-242-515-5605	Sequence 5605, Ap
604	200.2	22.1	650	17	US-10-027-632-197409	Sequence 197409,	677	199.8	22.0	2312	9	US-09-764-877-3606	Sequence 3606, Ap
605	200.2	22.1	650	17	US-10-027-632-197410	Sequence 197410,	678	199.8	22.0	2312	17	US-10-242-515-5606	Sequence 5606, Ap
606	200.2	22.1	701	13	US-10-027-632-13809	Sequence 13809, A	679	199.8	22.0	3364	20	US-10-723-860-7092	Sequence 7092, Ap
607	200.2	22.1	701	13	US-10-027-632-13810	Sequence 13810, A	680	199.8	22.0	10024	15	US-10-017-161-1671	Sequence 1671, Ap
608	200.2	22.1	701	17	US-10-027-632-13809	Sequence 13809, A	681	199.8	22.0	10102	17	US-10-292-798-1331	Sequence 1331, Ap
609	200.2	22.1	701	17	US-10-027-632-13810	Sequence 13810, A	682	199.8	22.0	18449	9	US-09-764-866-1457	Sequence 1457, Ap
610	200.2	22.1	1032	13	US-10-027-632-116774	Sequence 116774,	683	199.8	22.0	25668	13	US-10-087-192-1444	Sequence 1444, Ap
611	200.2	22.1	1032	13	US-10-027-632-116774	Sequence 116774,	684	199.8	22.0	27246	19	US-10-741-601-5676	Sequence 5676, Ap
612	200.2	22.1	31652	21	US-10-087-192-406	Sequence 406, App	685	199.8	22.0	27246	20	US-10-719-993-8851	Sequence 8851, Ap
613	200.2	22.1	35770	13	US-10-741-600-17693	Sequence 17693, A	686	199.8	22.0	28693	21	US-10-741-600-17761	Sequence 17761, Ap
614	200.2	22.1	59748	19	US-10-323-281-296	Sequence 296, App	687	199.8	22.0	44451	18	US-10-719-993-9361	Sequence 9361, Ap
615	200.2	22.1	106746	20	US-10-856-888-1	Sequence 1, Appl	688	199.8	22.0	94720	20	US-10-052-482-160	Sequence 160, App
616	200.2	22.1	106746	20	US-10-856-888-12	Sequence 12, Appl	689	199.8	22.0	122923	13	US-10-087-192-268	Sequence 268, App
617	200.2	22.1	113604	14	US-10-227-195A-1	Sequence 1, Appl	690	199.8	22.0	131673	22	US-10-723-860-4422	Sequence 4422, Ap
618	200.2	22.1	113604	14	US-10-227-195A-2	Sequence 2, Appl	691	199.8	22.0	131673	22	US-10-756-149-4416	Sequence 4416, Ap
619	200.2	22.1	113604	18	US-10-227-152B-1	Sequence 1, Appl	692	199.8	22.0	155937	20	US-10-723-860-2208	Sequence 2208, Ap
620	200.2	22.1	113604	18	US-10-227-152B-2	Sequence 2, Appl	693	199.8	22.0	160552	19	US-10-697-828-11	Sequence 11, Appl

694	199.8	22.0	170489	19	US-10-322-281-380	Sequence 380, App	6767	199	21.9	32816	9	US-09-729-094-3	Sequence 3, Appl1
695	199.8	22.0	174448	13	US-10-087-192-148	Sequence 148, App	6768	199	21.9	32816	16	US-10-435-631-3	Sequence 3, Appl1
696	199.6	22.0	712	17	US-10-027-632-151294	Sequence 151294, A	6769	199	21.9	33239	20	US-09-814-950-3	Sequence 3, Appl1
697	199.6	22.0	712	17	US-10-027-632-151294	Sequence 151294, A	6770	199	21.9	33239	20	US-10-472-442-3	Sequence 3, Appl1
698	199.6	22.0	1282	13	US-10-027-632-265009	Sequence 265009, A	6771	199	21.9	33982	21	US-10-369-626-3	Sequence 3, Appl1
699	199.6	22.0	1282	13	US-10-027-632-265009	Sequence 265009, A	6772	199	21.9	33982	21	US-10-900-420-3	Sequence 3, Appl1
700	199.6	22.0	2261	17	US-10-094-749-47	Sequence 47, Appl	6773	199	21.9	50927	13	US-10-367-094-56	Sequence 56, Appl
701	199.6	22.0	3178	13	US-10-027-632-113304	Sequence 113304, A	6774	199	21.9	126266	13	US-10-087-192-1132	Sequence 1132, Ap
702	199.6	22.0	3178	13	US-10-027-632-113304	Sequence 113304, A	6775	199	21.9	132762	10	US-09-954-556-17	Sequence 17, Appl
703	199.6	22.0	3262	13	US-10-098-841-83	Sequence 83, Appl	6776	199	21.9	133100	22	US-09-723-681-4	Sequence 4, Appl1
704	199.6	22.0	3406	13	US-10-027-632-11834	Sequence 11834, A	6777	199	21.9	148567	14	US-09-801-8768-3	Sequence 3, Appl1
705	199.6	22.0	3406	13	US-10-027-632-11834	Sequence 11834, A	6778	199	21.9	148567	14	US-10-254-869-3	Sequence 3, Appl1
706	199.6	22.0	3406	17	US-10-027-632-11834	Sequence 11834, A	6779	199	21.9	148567	18	US-10-667-442-3	Sequence 3, Appl1
707	199.6	22.0	3716	21	US-10-027-632-11835	Sequence 11835, A	6780	199	21.9	148567	21	US-10-965-635-3	Sequence 3, Appl1
708	199.6	22.0	4037	21	US-09-976-574-40	Sequence 40, Appl	6781	199	21.9	189063	21	US-10-484-577-69	Sequence 69, App
709	199.6	22.0	4037	21	US-09-976-574-40	Sequence 40, Appl	6782	199	21.9	196686	13	US-10-081-152-484	Sequence 484, App
710	199.6	22.0	4037	21	US-10-982-512-40	Sequence 40, Appl	6783	199	21.9	653122	13	US-10-087-192-226	Sequence 226, App
711	199.6	22.0	4076	21	US-09-976-574-32	Sequence 32, Appl	6784	199.8	21.9	362	13	US-10-027-632-255820	Sequence 255820, A
712	199.6	22.0	4076	21	US-10-982-512-32	Sequence 32, Appl	6785	199.8	21.9	362	13	US-10-027-632-31274	Sequence 31274, A
713	199.6	22.0	4120	21	US-09-976-574-38	Sequence 38, Appl	6786	199.8	21.9	972	13	US-10-027-632-31274	Sequence 31274, A
714	199.6	22.0	4120	21	US-10-982-512-38	Sequence 38, Appl	6787	199.8	21.9	972	13	US-10-027-632-31274	Sequence 31274, A
715	199.6	22.0	4159	21	US-09-976-574-30	Sequence 30, Appl	6788	199.8	21.9	2591	19	US-09-829-545-29	Sequence 29, Appl
716	199.6	22.0	4159	21	US-10-982-512-30	Sequence 30, Appl	6789	199.8	21.9	7152	20	US-10-668-800-29	Sequence 29, Appl
717	199.6	22.0	4180	9	US-09-976-574-36	Sequence 36, Appl	6790	199.8	21.9	21458	10	US-09-764-891-8810	Sequence 8810, Ap
718	199.6	22.0	4180	9	US-09-976-574-36	Sequence 36, Appl	6791	199.8	21.9	21470	9	US-09-764-847-1157	Sequence 1157, Ap
719	199.6	22.0	4219	21	US-09-976-574-28	Sequence 28, Appl	6792	199.8	21.9	21470	9	US-10-092-154-1157	Sequence 1157, Ap
720	199.6	22.0	4219	21	US-10-982-512-28	Sequence 28, Appl	6793	199.8	21.9	21666	14	US-10-052-482-208	Sequence 208, App
721	199.6	22.0	4263	9	US-09-976-574-34	Sequence 34, Appl	6794	199.8	21.9	21666	14	US-10-052-482-208	Sequence 208, App
722	199.6	22.0	4263	21	US-10-982-512-34	Sequence 34, Appl	6795	199.8	21.9	43950	9	US-09-735-9348-3	Sequence 3, Appl1
723	199.6	22.0	4302	21	US-09-976-574-24	Sequence 24, Appl	6796	199.8	21.9	43950	13	US-10-060-332-3	Sequence 3, Appl1
724	199.6	22.0	29534	20	US-10-719-993-6770	Sequence 6770, Ap	6797	199.8	21.9	43950	13	US-10-339-632-3	Sequence 3, Appl1
725	199.6	22.0	52745	19	US-10-741-601-5766	Sequence 5766, Ap	6798	199.8	21.9	43950	15	US-10-885-879-3	Sequence 3, Appl1
726	199.6	22.0	116704	13	US-10-087-192-1456	Sequence 1456, Ap	6799	199.8	21.9	51289	19	US-10-322-281-648	Sequence 648, App
727	199.6	22.0	116704	13	US-10-087-192-1456	Sequence 1456, Ap	6800	199.8	21.9	62658	19	US-10-322-281-648	Sequence 648, App
728	199.6	22.0	112976	19	US-10-367-094-99	Sequence 99, Appl	6801	199.8	21.9	70779	9	US-10-087-192-1012	Sequence 1012, Ap
729	199.6	22.0	181684	13	US-10-087-192-790	Sequence 790, Appl	6802	199.8	21.9	84539	13	US-09-962-436-36	Sequence 36, Appl
730	199.6	22.0	663	13	US-10-027-632-218457	Sequence 218457, A	6803	199.8	21.9	84539	21	US-10-843-6241A-2495	Sequence 2495, Ap
731	199.4	22.0	663	13	US-10-027-632-218457	Sequence 218457, A	6804	199.8	21.9	135289	21	US-10-240-422-1585	Sequence 1585, Ap
732	199.4	22.0	663	13	US-10-027-632-218457	Sequence 218457, A	6805	199.8	21.9	150288	22	US-10-981-277-52	Sequence 52, Appl
733	199.4	22.0	663	17	US-10-027-632-218458	Sequence 218458, A	6806	199.8	21.9	150288	22	US-10-981-277-52	Sequence 52, Appl
734	199.4	22.0	663	17	US-10-027-632-218458	Sequence 218458, A	6807	199.8	21.9	150288	22	US-10-981-277-52	Sequence 52, Appl
735	199.4	22.0	1664	17	US-09-764-877-2841	Sequence 2841, Ap	6808	199.8	21.9	34458	12	US-10-981-277-51	Sequence 51, Appl
736	199.4	22.0	1664	17	US-10-242-515-2841	Sequence 2841, Ap	6809	199.8	21.9	34458	12	US-10-087-192-334	Sequence 334, App
737	199.4	22.0	1756	14	US-10-108-2608A-2159	Sequence 2159, Ap	6810	199.8	21.9	34458	12	US-10-087-192-334	Sequence 334, App
738	199.4	22.0	6096	17	US-10-012-6008A-112	Sequence 112, App	6811	199.8	21.9	54605	20	US-10-719-993-8662	Sequence 8662, Ap
739	199.4	22.0	16815	13	US-10-017-161-1574	Sequence 1574, Ap	6812	199.8	21.9	473	13	US-10-674-124A-16624	Sequence 16624, A
740	199.4	22.0	33317	13	US-10-087-192-1714	Sequence 1714, Ap	6813	199.8	21.9	597	13	US-10-027-632-54449	Sequence 54449, A
741	199.4	22.0	41694	20	US-10-719-993-6806	Sequence 6806, Ap	6814	199.8	21.9	597	13	US-10-027-632-54449	Sequence 54449, A
742	199.4	22.0	49984	19	US-09-739-457-5	Sequence 5, Appl1	6815	199.8	21.9	597	13	US-10-027-632-54449	Sequence 54449, A
743	199.4	22.0	49984	19	US-09-739-457-5	Sequence 5, Appl1	6816	199.8	21.9	597	13	US-10-027-632-54449	Sequence 54449, A
744	199.4	22.0	52520	13	US-10-741-601-5700	Sequence 5700, Ap	6817	199.8	21.9	597	13	US-10-027-632-54449	Sequence 54449, A
745	199.4	22.0	138893	13	US-10-161-510-1	Sequence 1, Appl1	6818	199.8	21.9	1115	17	US-10-027-632-101064	Sequence 101064, A
746	199.4	22.0	220547	19	US-10-367-094-77	Sequence 77, Appl	6819	199.8	21.9	1115	17	US-10-027-632-101064	Sequence 101064, A
747	199.2	22.0	601	9	US-09-818-656A-61	Sequence 61, Appl	6820	199.8	21.9	1115	17	US-10-027-632-101064	Sequence 101064, A
748	199.2	22.0	21222	9	US-09-734-676-3	Sequence 3, Appl1	6821	199.8	21.9	1115	9	US-09-822-830A-379	Sequence 379, App
749	199.2	22.0	21222	16	US-10-388-415-3	Sequence 3, Appl1	6822	199.8	21.9	1946	15	US-10-037-270-462	Sequence 462, App
750	199.2	22.0	28588	14	US-09-764-887-399	Sequence 399, App	6823	199.8	21.9	1946	15	US-10-037-270-462	Sequence 462, App
751	199.2	22.0	28588	14	US-10-023-961-399	Sequence 399, App	6824	199.8	21.9	4963	17	US-09-764-877-2903	Sequence 2903, Ap
752	199.2	22.0	43853	13	US-10-322-281-788	Sequence 788, App	6825	199.8	21.9	4963	17	US-10-242-515-2903	Sequence 2903, Ap
753	199.2	22.0	61103	13	US-10-087-192-58	Sequence 58, Appl	6826	199.8	21.9	6096	9	US-09-764-864-1740	Sequence 1740, Ap
754	199.2	22.0	66973	13	US-10-087-192-574	Sequence 574, Appl	6827	199.8	21.9	15237	18	US-10-660-763-3	Sequence 3, Appl1
755	199.2	22.0	95001	17	US-10-174-020-11	Sequence 11, Appl	6828	199.8	21.9	15237	18	US-10-660-763-3	Sequence 3, Appl1
756	199.2	22.0	95929	11	US-09-997-722-88	Sequence 88, Appl	6829	199.8	21.9	18800	20	US-10-741-601-5764	Sequence 5764, Ap
757	199.2	22.0	597	17	US-10-027-632-294236	Sequence 294236, A	6830	199.8	21.9	18800	20	US-10-741-601-5764	Sequence 5764, Ap
758	199.2	22.0	597	17	US-10-027-632-294236	Sequence 294236, A	6831	199.8	21.9	30697	19	US-10-719-993-7044	Sequence 7044, Ap
759	199.2	22.0	604	13	US-10-027-632-152	Sequence 152, App	6832	199.8	21.9	32152	15	US-10-205-428-927	Sequence 927, App
760	199.2	22.0	604	13	US-10-027-632-152	Sequence 152, App	6833	199.8	21.9	32152	15	US-10-205-428-927	Sequence 927, App
761	199.2	22.0	11339	17	US-10-027-632-38633	Sequence 38633, A	6834	199.8	21.9	53226	9	US-09-818-664-3	Sequence 3, Appl1
762	199.2	22.0	11339	17	US-10-027-632-38633	Sequence 38633, A	6835	199.8	21.9	53226	9	US-09-818-664-3	Sequence 3, Appl1
763	199.2	22.0	3313	13	US-10-027-632-115534	Sequence 115534, A	6836	199.8	21.9	67088	19	US-10-473-339-3	Sequence 3, Appl1
764	199.2	22.0	3313	13	US-10-027-632-115534	Sequence 115534, A	6837	199.8	21.9	67088	19	US-10-473-339-3	Sequence 3, Appl1
765	199.2	22.0	21199	22	US-10-737-082-119	Sequence 119, App	6838	199.8	21.9	67088	21	US-10-741-601-5704	Sequence 5704, A
766	199.2	22.0	21199	22	US-10-765-790-119	Sequence 119, App	6839	199.8	21.9	76698	21	US-10-741-600-17804	Sequence 17804, A

840	198.6	21.9	76698	22	US-10-948-947A-1	Sequence 1, Appl1	c 913	198.2	21.9	18110	20	US-10-719-993-6766	Sequence 6766, Ap
841	198.6	21.9	86080	19	US-10-450-826-71	Sequence 71, Appl	c 914	198.2	21.9	21364	21	US-10-741-600-17782	Sequence 1782, A
842	198.6	21.9	86080	20	US-10-723-860-1697	Sequence 1697, Ap	c 915	198.2	21.9	29298	19	US-10-367-094-189	Sequence 189, App
843	198.6	21.9	86080	22	US-10-756-149-1653	Sequence 1653, Ap	c 916	198.2	21.9	32194	10	US-09-764-891-7028	Sequence 7028, Ap
844	198.6	21.9	106378	13	US-10-087-192-1624	Sequence 1624, Ap	c 917	198.2	21.9	37940	17	US-10-348-073A-12	Sequence 12, Appl
c 845	198.6	21.9	106707	19	US-10-694-685-8	Sequence 8, Appl1	c 918	198.2	21.9	38000	17	US-10-175-627-11	Sequence 11, Appl1
c 846	198.6	21.9	118466	21	US-10-461-862-86	Sequence 86, Appl	c 919	198.2	21.9	40887	19	US-10-741-601-5703	Sequence 5703, Ap
c 847	198.6	21.9	145806	20	US-10-719-993-6943	Sequence 6943, Ap	c 920	198.2	21.9	40987	21	US-10-741-600-18008	Sequence 18008, A
848	198.6	21.9	145831	9	US-09-969-708-79	Sequence 79, Appl	c 921	198.2	21.9	41866	13	US-10-087-192-1804	Sequence 1804, Ap
849	198.6	21.9	145831	10	US-09-954-456-2116	Sequence 2116, Ap	c 922	198.2	21.9	50000	17	US-10-364-505-7	Sequence 7, Appl1
850	198.6	21.9	145831	9	US-09-873-367C-646	Sequence 646, App	c 923	198.2	21.9	50000	19	US-10-681-199-7	Sequence 7, Appl1
851	198.6	21.9	145831	18	US-09-968-007A-455	Sequence 455, App	c 924	198.2	21.9	55346	20	US-10-719-993-7052	Sequence 7052, Ap
852	198.6	21.9	145831	11	US-10-240-425-363	Sequence 363, App	c 925	198.2	21.9	62124	20	US-10-417-375-82	Sequence 82, Appl
853	198.6	21.9	145831	21	US-10-843-641A-646	Sequence 646, App	c 927	198.2	21.9	115756	22	US-10-756-149-8838	Sequence 3838, Ap
854	198.6	21.9	145831	21	US-10-843-641A-5143	Sequence 5143, Ap	c 927	198.2	21.9	12326	22	US-09-910-185-11	Sequence 11, Appl
855	198.6	21.9	145831	21	US-10-843-641A-5925	Sequence 6925, Ap	c 928	198.2	21.9	202814	20	US-10-719-993-6812	Sequence 6812, Ap
856	198.6	21.9	145831	21	US-10-843-641A-7550	Sequence 7550, Ap	c 929	198.2	21.9	246640	19	US-10-332-666-58	Sequence 58, Appl
857	198.6	21.9	145831	22	US-10-756-149-921	Sequence 921, App	c 930	198.2	21.9	317876	21	US-10-741-601-5629	Sequence 5629, Ap
858	198.6	21.9	154875	22	US-10-737-082-107	Sequence 107, App	c 931	198.2	21.9	317876	21	US-10-741-600-17607	Sequence 17607, A
859	198.6	21.9	154875	22	US-10-765-799-107	Sequence 107, App	c 932	198.2	21.9	368004	9	US-09-949-654-3	Sequence 3, Appl1
860	198.6	21.9	36803	20	US-10-719-993-6805	Sequence 6805, Ap	c 933	198.2	21.9	383432	22	US-10-737-082-34	Sequence 34, Appl
c 861	198.6	21.9	410846	21	US-10-481-613-1	Sequence 1, Appl1	c 934	198.2	21.9	383432	22	US-10-765-799-34	Sequence 1463, Ap
c 862	198.4	21.9	291	16	US-10-229-058B-15	Sequence 15, Appl	c 936	198.2	21.9	418550	20	US-10-719-993-6817	Sequence 6817, Ap
c 863	198.4	21.9	638	13	US-10-027-632-234365	Sequence 234365,	c 937	198.2	21.8	493	22	US-10-933-118-33	Sequence 33, Appl
c 864	198.4	21.9	638	13	US-10-027-632-234366	Sequence 234366,	c 938	198.2	21.8	572	13	US-10-027-632-187116	Sequence 187116,
c 865	198.4	21.9	638	13	US-10-027-632-234367	Sequence 234367,	c 939	198.2	21.8	572	13	US-10-027-632-187116	Sequence 187116,
c 866	198.4	21.9	638	13	US-10-027-632-234368	Sequence 234368,	c 940	198.2	21.8	572	13	US-10-027-632-187116	Sequence 187116,
c 867	198.4	21.9	638	13	US-10-027-632-234369	Sequence 234369,	c 941	198.2	21.8	705	13	US-10-027-632-142951	Sequence 142951,
c 868	198.4	21.9	638	17	US-10-027-632-234365	Sequence 234365,	c 942	198.2	21.8	825	13	US-10-027-632-142951	Sequence 142951,
c 869	198.4	21.9	638	17	US-10-027-632-234366	Sequence 234366,	c 943	198.2	21.8	825	13	US-10-027-632-169285	Sequence 169285,
c 870	198.4	21.9	638	17	US-10-027-632-234367	Sequence 234367,	c 944	198.2	21.8	1204	13	US-10-027-632-169285	Sequence 169285,
c 871	198.4	21.9	638	17	US-10-027-632-234368	Sequence 234368,	c 945	198.2	21.8	1204	13	US-10-027-632-118994	Sequence 118994,
c 872	198.4	21.9	638	17	US-10-027-632-234369	Sequence 234369,	c 946	198.2	21.8	1204	17	US-10-027-632-118994	Sequence 118994,
873	198.4	21.9	826	17	US-10-027-632-8234	Sequence 8234, Ap	c 947	198.2	21.8	1204	17	US-10-027-632-118994	Sequence 118994,
874	198.4	21.9	826	17	US-10-027-632-8234	Sequence 8234, Ap	c 948	198.2	21.8	2460	20	US-10-723-860-7028	Sequence 7028, Ap
875	198.4	21.9	1295	13	US-10-027-632-133215	Sequence 133215,	c 949	198.2	21.8	3448	13	US-10-108-260A-595	Sequence 595, App
876	198.4	21.9	1295	13	US-10-027-632-133216	Sequence 133216,	c 950	198.2	21.8	3448	17	US-10-027-632-115054	Sequence 115054,
877	198.4	21.9	1295	13	US-10-027-632-133217	Sequence 133217,	c 951	198.2	21.8	9432	14	US-10-942-310-1	Sequence 1, Appl1
878	198.4	21.9	1295	17	US-10-027-632-133215	Sequence 133215,	c 952	198.2	21.8	9432	18	US-10-712-363-1	Sequence 1, Appl1
879	198.4	21.9	1295	17	US-10-027-632-133216	Sequence 133216,	c 953	198.2	21.8	9432	18	US-10-712-363-1	Sequence 1, Appl1
880	198.4	21.9	1295	17	US-10-027-632-133217	Sequence 133217,	c 954	198.2	21.8	9432	18	US-10-712-363-1	Sequence 1, Appl1
881	198.4	21.9	1672	9	US-09-764-847-1183	Sequence 1183, Ap	c 955	198.2	21.8	9609	21	US-10-635-780-4	Sequence 4, Appl1
882	198.4	21.9	1672	14	US-10-092-154-1183	Sequence 1183, Ap	c 956	198.2	21.8	11557	9	US-09-764-856-103	Sequence 103, App
c 883	198.4	21.9	2549	17	US-10-108-260A-413	Sequence 1413, Ap	c 957	198.2	21.8	11557	10	US-09-764-856-103	Sequence 104, App
c 884	198.4	21.9	3310	22	US-10-756-149-592	Sequence 592, App	c 958	198.2	21.8	11557	10	US-09-764-856-103	Sequence 104, App
885	198.4	21.9	22186	21	US-10-085-117-178	Sequence 178, App	c 959	198.2	21.8	11557	11	US-09-764-856-103	Sequence 104, App
886	198.4	21.9	23013	17	US-10-741-600-17898	Sequence 17898, A	c 960	198.2	21.8	11557	11	US-09-764-856-103	Sequence 104, App
887	198.4	21.9	25322	21	US-10-741-600-17737	Sequence 17737, A	c 961	198.2	21.8	11557	14	US-10-102-627-103	Sequence 103, Appl
888	198.4	21.9	86081	19	US-10-741-601-5640	Sequence 5640, Ap	c 962	198.2	21.8	11557	14	US-10-102-627-103	Sequence 103, Appl
889	198.4	21.9	86081	23	US-10-741-600-17633	Sequence 17633, A	c 963	198.2	21.8	11557	9	US-09-764-864-1698	Sequence 1698, Ap
c 890	198.4	21.9	87867	13	US-10-087-192-1878	Sequence 192, App	c 964	198.2	21.8	32134	10	US-09-764-864-1698	Sequence 1698, Ap
891	198.4	21.9	87869	19	US-10-717-597-194	Sequence 194, App	c 965	198.2	21.8	32134	15	US-10-205-428-508	Sequence 608, App
892	198.4	21.9	95835	13	US-10-087-192-1792	Sequence 1792, App	c 966	198.2	21.8	32134	15	US-10-205-428-508	Sequence 608, App
893	198.4	21.9	128034	17	US-10-283-174-187	Sequence 187, App	c 967	198.2	21.8	32191	15	US-10-205-428-508	Sequence 609, App
894	198.4	21.9	128034	21	US-10-600-009-187	Sequence 187, App	c 968	198.2	21.8	32191	15	US-10-205-428-508	Sequence 609, App
895	198.4	21.9	143899	21	US-09-972-546-15	Sequence 15, Appl	c 969	198.2	21.8	39898	21	US-10-741-600-17692	Sequence 17692, A
896	198.4	21.9	143899	21	US-10-735-256-15	Sequence 15, Appl	c 970	198.2	21.8	40000	21	US-10-741-600-18015	Sequence 18015, A
897	198.4	21.9	174424	9	US-09-967-768A-314	Sequence 314, App	c 971	198.2	21.8	40045	9	US-09-818-656A-3	Sequence 3, Appl1
898	198.4	21.9	174424	10	US-09-960-706-969	Sequence 969, App	c 972	198.2	21.8	40045	9	US-09-818-656A-3	Sequence 3, Appl1
899	198.4	21.9	174424	21	US-10-843-641A-6459	Sequence 6459, Ap	c 973	198.2	21.8	40045	22	US-10-961-230-3	Sequence 3, Appl1
900	198.4	21.9	181343	21	US-10-723-860-2392	Sequence 2392, Ap	c 974	198.2	21.8	55114	22	US-10-087-192-1606	Sequence 1606, Ap
901	198.4	21.9	181343	22	US-10-756-149-2215	Sequence 2215, Ap	c 975	198.2	21.8	59817	18	US-10-052-482-190	Sequence 190, App
902	198.4	21.9	203654	22	US-09-820-905-3	Sequence 3, Appl1	c 976	198.2	21.8	70000	20	US-10-476-991-3	Sequence 3, Appl1
903	198.4	21.9	203654	22	US-10-473-338A-3	Sequence 3, Appl1	c 977	198.2	21.8	73771	13	US-10-087-192-1636	Sequence 1636, Ap
904	198.2	21.9	1326	13	US-10-027-632-123225	Sequence 123225,	c 978	198.2	21.8	110665	22	US-10-723-860-0002	Sequence 2002, Ap
905	198.2	21.9	1326	13	US-10-027-632-123226	Sequence 123226,	c 979	198.2	21.8	110665	22	US-10-723-860-0002	Sequence 2002, Ap
906	198.2	21.9	1326	17	US-10-027-632-133225	Sequence 133225,	c 980	198.2	21.8	114771	20	US-10-723-860-058	Sequence 458, App
907	198.2	21.9	1326	17	US-10-027-632-133226	Sequence 133226,	c 981	198.2	21.8	132762	17	US-10-954-556-17	Sequence 17, Appl
908	198.2	21.9	2062	17	US-10-108-260A-1541	Sequence 1541, Ap	c 982	198.2	21.8	149671	17	US-10-226-031B-53	Sequence 53, Appl
909	198.2	21.9	2541	9	US-09-823-245A-569	Sequence 569, App	c 983	198.2	21.8	159204	22	US-10-756-149-8804	Sequence 3804, Ap
910	198.2	21.9	4824	9	US-09-960-253-160	Sequence 160, App	c 984	198.2	21.8	410846	21	US-10-481-613-1	Sequence 1, Appl1
911	198.2	21.9	4824	15	US-10-171-581-82	Sequence 82, Appl	c 985	197.8	21.8	606398	20	US-10-719-993-6782	Sequence 6782, Ap
912	198.2	21.9	4885	22	US-10-220-335-81	Sequence 81, Appl	c 985	197.8	21.8	648	13	US-10-027-632-107015	Sequence 107015,

c986	197.8	21.8	648	17	US-10-027-632-107015	Sequence 107015, Appl1	1059	197.4	21.8	1449	21	US-10-087-155A-909	Sequence 909, Appl
c987	197.8	21.8	1167	22	US-10-499-353A-2	Sequence 2, Appl1	1060	197.4	21.8	1449	21	US-10-156-251-2117	Sequence 2117, Appl
c988	197.8	21.8	3129	9	US-09-735-103-9	Sequence 9, Appl1	1061	197.4	21.8	1599	19	US-10-153-668-439	Sequence 439, Appl
c989	197.8	21.8	3129	13	US-10-045-488A-79	Sequence 9, Appl1	c1062	197.4	21.8	14963	19	US-10-741-601-5776	Sequence 5776, Appl
c990	197.8	21.8	3705	13	US-09-822-846-79	Sequence 279, Appl	c1063	197.4	21.8	23459	19	US-10-741-601-5699	Sequence 5699, Appl
c991	197.8	21.8	6510	13	US-10-098-841-139	Sequence 139, Appl	c1064	197.4	21.8	33175	19	US-10-741-601-5651	Sequence 5651, Appl
c992	197.8	21.8	21913	10	US-09-764-891-6065	Sequence 6065, Ap	c1065	197.4	21.8	45656	20	US-10-719-993-6610	Sequence 6610, Appl
c993	197.8	21.8	21913	10	US-09-764-891-6066	Sequence 6066, Ap	c1066	197.4	21.8	52710	19	US-10-322-281-512	Sequence 512, Appl
c994	197.8	21.8	21913	10	US-09-764-891-6067	Sequence 6067, Ap	c1067	197.4	21.8	61765	19	US-10-322-281-512	Sequence 512, Appl
c995	197.8	21.8	25001	17	US-10-187-659A-11	Sequence 11, Appl1	c1068	197.4	21.8	68255	13	US-10-087-192-779	Sequence 779, Appl
c996	197.8	21.8	28616	17	US-10-455-552-1	Sequence 1, Appl1	c1069	197.4	21.8	117231	22	US-10-089-313-139	Sequence 314, Appl
c997	197.8	21.8	32191	17	US-10-074-024-446	Sequence 446, Appl	c1070	197.4	21.8	174424	9	US-09-960-704A-969	Sequence 969, Appl
c998	197.8	21.8	32865	13	US-10-087-192-964	Sequence 964, Appl	c1071	197.4	21.8	174424	21	US-10-843-631A-9459	Sequence 6459, Appl
c999	197.8	21.8	53522	13	US-09-904-968A-1	Sequence 1, Appl1	c1072	197.4	21.8	174424	21	US-10-723-670-1	Sequence 2392, Appl
c999	197.8	21.8	70322	13	US-10-087-192-1294	Sequence 1294, Ap	c1073	197.4	21.8	181343	22	US-10-723-670-1	Sequence 2392, Appl
c1000	197.8	21.8	96356	19	US-10-087-169-352	Sequence 352, Appl	c1074	197.4	21.8	181343	22	US-10-756-149-2215	Sequence 2215, Appl
c1001	197.8	21.8	96356	19	US-10-775-169-352	Sequence 352, Appl	c1075	197.4	21.8	181343	22	US-10-756-149-2215	Sequence 2215, Appl
c1002	197.8	21.8	98716	21	US-10-741-600-17754	Sequence 17754, A	c1076	197.4	21.8	187844	20	US-10-719-993-6683	Sequence 6683, Appl
c1003	197.8	21.8	103660	21	US-10-741-600-17645	Sequence 17645, A	c1077	197.4	21.8	214000	21	US-10-829-697-1	Sequence 1, Appl1
c1004	197.8	21.8	113000	16	US-10-376-566-16	Sequence 16, Appl1	c1078	197.4	21.8	214000	21	US-10-830-477-1	Sequence 1, Appl1
c1005	197.8	21.8	128034	17	US-10-282-174-186	Sequence 186, Appl	c1079	197.4	21.8	447894	9	US-10-723-670-1	Sequence 1, Appl1
c1006	197.8	21.8	128034	21	US-10-600-009-186	Sequence 186, Appl	c1080	197.4	21.8	447894	21	US-09-933-2678A-1	Sequence 3327, Appl
c1007	197.8	21.8	128034	13	US-10-087-192-340	Sequence 340, Appl	c1081	197.2	21.7	402	19	US-10-674-128A-386	Sequence 386, Appl
c1008	197.8	21.8	134592	18	US-10-240-425-1102	Sequence 1102, Ap	c1082	197.2	21.7	600	21	US-10-956-157-7721	Sequence 7721, Appl
c1009	197.8	21.8	134592	21	US-10-278-698-335	Sequence 335, Appl	c1083	197.2	21.7	648	13	US-10-027-632-112653	Sequence 112653, Appl
c1010	197.8	21.8	134592	21	US-10-278-698-335	Sequence 849, Appl	c1084	197.2	21.7	648	13	US-10-027-632-112653	Sequence 112653, Appl
c1011	197.8	21.8	162450	15	US-10-071-179-1	Sequence 1, Appl1	c1085	197.2	21.7	648	17	US-10-027-632-112654	Sequence 112654, Appl
c1012	197.8	21.8	162450	15	US-10-126-704-1	Sequence 1, Appl1	c1086	197.2	21.7	751	10	US-09-953-318-20	Sequence 20, Appl1
c1013	197.8	21.8	202100	17	US-10-282-174-184	Sequence 484, Appl	c1087	197.2	21.7	751	17	US-10-446-337-20	Sequence 20, Appl1
c1014	197.8	21.8	202100	21	US-10-600-009-484	Sequence 6799, Ap	c1088	197.2	21.7	854	13	US-10-027-632-167774	Sequence 162774, Appl
c1015	197.8	21.8	255339	20	US-10-719-993-6799	Sequence 33, Appl1	c1089	197.2	21.7	854	13	US-10-027-632-167774	Sequence 162774, Appl
c1016	197.8	21.8	300000	15	US-10-262-552-33	Sequence 33, Appl1	c1090	197.2	21.7	2092	21	US-10-956-157-2486	Sequence 2486, Appl
c1017	197.8	21.8	300000	19	US-10-703-210-33	Sequence 33, Appl1	c1091	197.2	21.7	6658	21	US-09-764-891-5709	Sequence 5709, Appl
c1018	197.8	21.8	325791	11	US-09-768-185A-1	Sequence 1, Appl1	c1092	197.2	21.7	8577	19	US-09-764-891-8855	Sequence 8855, Appl
c1019	197.6	21.8	601	9	US-09-818-656A-60	Sequence 60, Appl1	c1093	197.2	21.7	33478	19	US-10-322-281-188	Sequence 188, Appl
c1020	197.6	21.8	601	9	US-09-818-656A-62	Sequence 62, Appl1	c1094	197.2	21.7	35804	21	US-10-898-406-3	Sequence 3, Appl1
c1021	197.6	21.8	2702	10	US-09-822-846-142	Sequence 142, Appl	c1095	197.2	21.7	40433	22	US-09-880-107-3327	Sequence 3327, Ap
c1022	197.6	21.8	12586	21	US-10-741-600-171608	Sequence 17608, A	c1096	197.2	21.7	40433	22	US-10-756-149-1455	Sequence 1455, Appl
c1023	197.6	21.8	23526	9	US-09-764-878-261	Sequence 261, Appl	c1097	197.2	21.7	57759	18	US-10-783-271-108	Sequence 108, Appl
c1024	197.6	21.8	23526	9	US-09-764-878-261	Sequence 940, Appl	c1098	197.2	21.7	57759	18	US-10-052-482-34	Sequence 34, Appl
c1025	197.6	21.8	23526	14	US-10-079-854-261	Sequence 261, Appl	c1099	197.2	21.7	70000	17	US-10-010-622-13	Sequence 13, Appl1
c1026	197.6	21.8	23526	14	US-10-074-095-940	Sequence 940, Appl	c1100	197.2	21.7	70000	17	US-10-010-622-13	Sequence 13, Appl1
c1027	197.6	21.8	23526	17	US-10-212-872-940	Sequence 940, Appl	c1101	197.2	21.7	92139	16	US-09-918-686-1	Sequence 1, Appl1
c1028	197.6	21.8	23526	17	US-10-212-872-940	Sequence 940, Appl	c1102	197.2	21.7	92139	16	US-10-953-150-1	Sequence 1, Appl1
c1029	197.6	21.8	23526	9	US-09-764-878-262	Sequence 262, Appl	c1103	197.2	21.7	130320	22	US-10-408-168-1	Sequence 1, Appl1
c1030	197.6	21.8	23526	14	US-10-079-854-262	Sequence 262, Appl	c1104	197.2	21.7	166496	22	US-10-756-149-590	Sequence 590, Appl
c1031	197.6	21.8	23526	14	US-10-074-095-941	Sequence 941, Appl	c1105	197.2	21.7	166496	22	US-10-052-482-34	Sequence 42, Appl
c1032	197.6	21.8	23526	17	US-10-212-872-941	Sequence 941, Appl	c1106	197.2	21.7	166496	22	US-10-981-277-42	Sequence 17765, A
c1033	197.6	21.8	23526	17	US-10-034-650-58	Sequence 58, Appl1	c1107	197.2	21.7	317129	21	US-10-741-600-17765	Sequence 250, Appl
c1034	197.6	21.8	23526	17	US-10-034-650-58	Sequence 76, Appl1	c1108	197.2	21.7	317129	21	US-10-087-192-250	Sequence 3, Appl1
c1035	197.6	21.8	23526	13	US-10-087-192-1030	Sequence 1030, Ap	c1109	197.2	21.7	567564	19	US-10-699-156-3	Sequence 104432, Appl
c1036	197.6	21.8	52967	19	US-10-322-281-386	Sequence 386, Appl	c1110	197.2	21.7	705	13	US-10-027-632-142952	Sequence 325526, Appl
c1037	197.6	21.8	52967	19	US-10-741-601-5775	Sequence 5775, Ap	c1111	197.2	21.7	705	13	US-10-027-632-142952	Sequence 325526, Appl
c1038	197.6	21.8	52967	19	US-10-741-601-5775	Sequence 5775, Ap	c1112	197.2	21.7	705	13	US-10-027-632-142952	Sequence 325526, Appl
c1039	197.6	21.8	52967	19	US-10-741-601-5775	Sequence 5775, Ap	c1113	197.2	21.7	705	13	US-10-027-632-142952	Sequence 325526, Appl
c1040	197.6	21.8	175737	20	US-10-723-860-1153	Sequence 1153, Ap	c1114	197.2	21.7	705	17	US-10-027-632-142952	Sequence 325526, Appl
c1041	197.6	21.8	175737	20	US-10-723-860-1153	Sequence 34, Appl1	c1115	197.2	21.7	1515	17	US-10-074-424-684	Sequence 684, Appl
c1042	197.6	21.8	175737	22	US-10-783-271-34	Sequence 34, Appl1	c1116	197.2	21.7	2818	20	US-10-602-494-28	Sequence 28, Appl1
c1043	197.6	21.8	198532	13	US-10-087-192-24	Sequence 24, Appl	c1117	197.2	21.7	2818	20	US-10-602-494-28	Sequence 28, Appl1
c1044	197.6	21.8	198532	13	US-10-087-192-24	Sequence 24, Appl	c1118	197.2	21.7	2818	20	US-10-602-494-28	Sequence 28, Appl1
c1045	197.6	21.8	260209	15	US-10-265-071-22	Sequence 23, Appl1	c1119	197.2	21.7	2818	15	US-10-602-494-28	Sequence 301, Appl
c1046	197.6	21.8	260209	15	US-10-265-071-22	Sequence 23, Appl1	c1120	197.2	21.7	2818	15	US-10-602-494-28	Sequence 301, Appl
c1047	197.4	21.8	463	19	US-09-731-231A-3	Sequence 3, Appl1	c1121	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1048	197.4	21.8	463	19	US-09-731-231A-3	Sequence 3, Appl1	c1122	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1049	197.4	21.8	463	19	US-09-731-231A-3	Sequence 3, Appl1	c1123	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1050	197.4	21.8	463	19	US-09-731-231A-3	Sequence 3, Appl1	c1124	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1051	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1125	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1052	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1126	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1053	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1127	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1054	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1128	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1055	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1129	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1056	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1130	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1057	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1131	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1058	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1132	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1059	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1133	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1060	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1134	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
c1061	197.4	21.8	600	21	US-10-956-157-7352	Sequence 7352, Ap	c1135	197.2	21.7	8397	20	US-10-017-375-12	Sequence 37, Appl1
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c1134	197	21.7	116792	13	US-10-087-192-1090	Sequence 1090, Ap
c1135	197	21.7	119501	17	US-10-174-319-15	Sequence 15, Appl
c1136	197	21.7	119596	14	US-10-270-336-3	Sequence 3, Appl1
c1137	197	21.7	128034	17	US-10-282-174-166	Sequence 186, App
c1138	197	21.7	128034	17	US-10-282-174-187	Sequence 187, App
c1139	197	21.7	128034	21	US-10-600-009-186	Sequence 186, App
c1140	197	21.7	128034	21	US-10-600-009-187	Sequence 187, App
c1141	197	21.7	136436	22	US-10-756-149-3773	Sequence 3773, Ap
c1142	197	21.7	155074	13	US-10-026-188-6	Sequence 6, Appl1
c1143	197	21.7	166181	20	US-10-723-860-1452	Sequence 1452, Ap
c1144	197	21.7	166181	20	US-10-723-860-3281	Sequence 3281, Ap
c1145	197	21.7	174448	13	US-10-087-192-148	Sequence 148, App
c1146	197	21.7	193691	20	US-10-719-993-6768	Sequence 6768, Ap
c1147	197	21.7	212231	13	US-10-087-192-1126	Sequence 1126, Ap
c1148	197	21.7	231914	21	US-10-741-600-17654	Sequence 17654, A
c1149	197	21.7	275449	13	US-10-087-192-520	Sequence 520, App
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c1151	196.8	21.7	887	13	US-10-027-632-156973	Sequence 156974,
c1152	196.8	21.7	887	13	US-10-027-632-156974	Sequence 156975,
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c1154	196.8	21.7	887	17	US-10-027-632-156973	Sequence 156974,
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c1156	196.8	21.7	943	13	US-10-027-632-122182	Sequence 122182,
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c1158	196.8	21.7	2308	17	US-10-104-047-682	Sequence 682, App
c1159	196.8	21.7	2404	17	US-10-108-260A-1180	Sequence 1180, Ap
c1160	196.8	21.7	6833	20	US-10-723-860-6965	Sequence 6965, Ap
c1161	196.8	21.7	6833	20	US-10-723-860-7739	Sequence 7739, Ap
c1162	196.8	21.7	7444	10	US-09-764-891-8806	Sequence 8806, Ap
c1163	196.8	21.7	7444	10	US-09-764-891-9448	Sequence 9448, Ap
c1164	196.8	21.7	7444	9	US-10-091-414-316	Sequence 316, App
c1165	196.8	21.7	9765	9	US-09-764-853-888	Sequence 888, App
c1166	196.8	21.7	9765	9	US-09-764-853-935	Sequence 935, App
c1167	196.8	21.7	9765	14	US-10-091-438-248	Sequence 248, App
c1168	196.8	21.7	9765	14	US-10-091-438-257	Sequence 257, App
c1169	196.8	21.7	21704	15	US-10-017-161-709	Sequence 709, App
c1170	196.8	21.7	21704	17	US-10-292-798-621	Sequence 621, App
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c1172	196.8	21.7	32192	9	US-09-764-877-3657	Sequence 3657, Ap
c1173	196.8	21.7	32192	9	US-09-764-891-9791	Sequence 9791, Ap
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c1175	196.8	21.7	35641	9	US-09-962-436-306	Sequence 306, App
c1176	196.8	21.7	35641	9	US-09-880-107-2225	Sequence 2225, Ap
c1177	196.8	21.7	35641	21	US-10-843-641A-2765	Sequence 2765, Ap
c1178	196.8	21.7	37925	11	US-09-984-429-701	Sequence 701, App
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c1180	196.8	21.7	44325	11	US-09-997-722-226	Sequence 226, App
c1181	196.8	21.7	45944	19	US-10-367-094-38	Sequence 38, Appl
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c1183	196.8	21.7	67253	22	US-10-737-082-88	Sequence 88, Appl
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c1188	196.8	21.7	106938	19	US-10-322-281-566	Sequence 566, App
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c1190	196.8	21.7	145806	20	US-10-719-993-6943	Sequence 6943, Ap
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c1192	196.8	21.7	165097	22	US-10-737-082-77	Sequence 77, Appl
c1193	196.8	21.7	165097	22	US-10-765-790-77	Sequence 77, Appl
c1194	196.8	21.7	201239	21	US-10-278-698-246	Sequence 246, App
c1195	196.8	21.7	201239	21	US-10-278-698-760	Sequence 760, App
c1196	196.8	21.7	201239	21	US-10-719-993-6876	Sequence 6876, Ap
c1197	196.8	21.7	606398	20	US-10-719-993-6782	Sequence 6782, Ap
c1198	196.6	21.7	288	14	US-10-115-278-2	Sequence 2, Appl1
c1199	196.6	21.7	288	10	US-10-762-966-2	Sequence 2, Appl1
c1200	196.6	21.7	461	9	US-09-884-441-1	Sequence 1, Appl1
c1201	196.6	21.7	461	9	US-09-884-441-3	Sequence 3, Appl1
c1202	196.6	21.7	461	10	US-09-907-969-1	Sequence 1, Appl1
c1203	196.6	21.7	461	10	US-09-907-969-3	Sequence 3, Appl1
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Search completed: September 15, 2005, 20:27:59
Job time : 867 secs

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c1207	196.6	21.7	461	21	US-10-129-053-3	Sequence 3, Appl1
c1208	196.6	21.7	461	21	US-10-860-790-1	Sequence 1, Appl1
c1209	196.6	21.7	461	21	US-10-860-790-3	Sequence 3, Appl1
c1210	196.6	21.7	571	13	US-10-027-632-252752	Sequence 252752,
c1211	196.6	21.7	571	17	US-10-027-632-252752	Sequence 252752,
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Run on: September 15, 2005, 13:47:33 ; Search time 617 Seconds
(without alignments)
8702.116 Million cell updates/sec

Title: US-09-989-733-398
Perfect score: 1 ggaactctgaaggtcccaagc.....gtgagactcaccctcacaca 907
Sequence: IDENTITY_NOC
Scoring table: Gapop 10.0 , Gapext 1.0
Gapop 10.0 , Gapext 1.0

Searched: 4390206 segs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : N_Geneseq_16Dec04:*
1: geneseq119808:*
2: geneseq119908:*
3: geneseq120008:*
4: geneseq120018:*
5: geneseq120028:*
6: geneseq120038:*
7: geneseq120048:*
8: geneseq120058:*
9: geneseq120068:*
10: geneseq120078:*
11: geneseq120088:*
12: geneseq120098:*
13: geneseq120108:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAZ65100	standard;	CDNA;	907	BP.	
DE	Membrane-bound protein PRO1187	encoding	CDNA.			
PN	WO963088-A2.					
PD	03-DEC-1999.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 3;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 2						
ID	AAC58387	standard;	CDNA;	907	BP.	
DE	Human PRO1187	nucleotide	sequence	SEQ ID NO:54.		
PN	WO200053755-A2.					
PD	14-SEP-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 3;	Length 907;	
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RESULT 3						
ID	AAFA4446	standard;	CDNA;	907	BP.	
DE	Human PRO1187	(UNQ601)	nucleotide	sequence	SEQ ID NO:398.	
PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 5;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 4						
ID	ABK33584	standard;	CDNA;	907	BP.	
DE	CDNA encoding human PRO	protein, Seq ID NO 97.				
PN	WO200208288-A2.					
PD	31-JAN-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 6;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 5						
ID	ACA64425	standard;	CDNA;	907	BP.	
DE	Novel human secreted and transmembrane	protein PRO1187	CDNA.			
PN	US2003003531-A1.					
PD	02-JAN-2003.					
PA	(GETH) GENENTECH INC.					

Query Match		100.0%;	Score 907;	DB 8;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 6						
ID	ABX80884	standard;	CDNA;	907	BP.	
DE	Human secreted/transmembrane	protein CDNA, #160.				
PN	US2003027162-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 8;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 7						
ID	ACD44393	standard;	CDNA;	907	BP.	
DE	CDNA encoding human PRO1187	polypeptide.				
PN	US2002127576-A1.					
PD	12-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 8;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 8						
ID	ACA68545	standard;	CDNA;	907	BP.	
DE	Novel human secreted and transmembrane	protein PRO1187	CDNA.			
PN	US2003088063-A1.					
PD	08-MAY-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 8;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 9						
ID	ABX79564	standard;	CDNA;	907	BP.	
DE	Human secreted/transmembrane	protein CDNA, #160.				
PN	US2002142961-A1.					
PD	03-OCT-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 8;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 10						
ID	ACA93585	standard;	CDNA;	907	BP.	
DE	Novel human secreted and transmembrane	protein PRO1187	CDNA.			
PN	US2003022187-A1.					
PD	30-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 8;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 11						
ID	ABX81267	standard;	DNA;	907	BP.	
DE	Novel human secreted or transmembrane	protein PRO1185	DNA.			
PN	US2003027985-A1.					
PD	06-FEB-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 8;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 12						
ID	ACA93083	standard;	CDNA;	907	BP.	
DE	Novel human secreted and transmembrane	protein PRO1187	CDNA.			
PN	US2003017476-A1.					
PD	23-JAN-2003.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 8;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 13						
ID	ABX17167	standard;	CDNA;	907	BP.	
DE	Human PRO	polynucleotide #124.				
PN	US2002123463-A1.					
PD	05-SEP-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 8;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 14						
ID	ACA68022	standard;	CDNA;	907	BP.	
DE	Novel human secreted and transmembrane	protein PRO1187	CDNA.			
PN	US2002177164-A1.					
PD	28-NOV-2002.					
PA	(GETH) GENENTECH INC.					
Query Match		100.0%;	Score 907;	DB 9;	Length 907;	
Best Local Similarity		100.0%;	Pred. No. 2.6e-250;			
RESULT 15						
ID	ACA88471	standard;	CDNA;	907	BP.	
DE	Human secreted and transmembrane	polypeptide PRO1187	CDNA.			

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PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 16
ID ACD81978 standard; cDNA; 907 BP.
DE cDNA encoding human PRO1187 polypeptide.
PN US2003017981-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 17
ID ABT44274 standard; cDNA; 907 BP.
DE Human PRO1187 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 18
ID ADA37909 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003008297-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 19
ID ADA21595 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1187.
PN US2003054404-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 20
ID ADA10382 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO1187.
PN US2003059831-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 21
ID ADA17926 standard; cDNA; 907 BP.
DE cDNA encoding human PRO1187 polypeptide.
PN US2003054987-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 22
ID ADA28034 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003054359-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 23
ID ADA9614 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003059832-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 24
ID ADA3839 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 25
ID ABT44557 standard; cDNA; 907 BP.
DE Human PRO1187 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 26
ID ADA92960 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 27
ID ACD82224 standard; cDNA; 907 BP.
DE Human secreted/transmembrane polypeptide PRO 1187 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 28
ID ACH65539 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003044806-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 29
ID ADA22521 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1187.
PN US2003040473-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 30
ID ACD39529 standard; cDNA; 907 BP.
DE Human cDNA encoding PRO1185.
PN US2003017982-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 31
ID ADA06687 standard; cDNA; 907 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #124.
PN US2003049638-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 32
ID ABT43930 standard; cDNA; 907 BP.
DE Human membrane bound receptor/protein PRO1187 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 33
ID ADA39380 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003059782-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 34
ID ADB83587 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 35
ID ADB80693 standard; cDNA; 907 BP.
```

DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 36
ID ADB73234 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003086968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 37
ID ADB96406 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 38
ID ADB78316 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 9; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 39
ID ADB84964 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 40
ID ADB78070 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 41
ID ADB87136 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 42
ID ADB84718 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 43
ID ADB83833 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 44
ID ADB72988 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003092887-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 45
ID ADC57878 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003027754-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 46
ID ADC55242 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003045463-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 47
ID ADC12109 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003049681-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 48
ID ADC56531 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003064375-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 49
ID ADC07586 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003068647-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 50
ID ADC11576 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003068403-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 51
ID ADC36826 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 52
ID ADC21816 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 53
ID ADC49847 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 54
ID ADC49046 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.

PN US2003088070-A1.
PD 08-MAY-2003.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 55
ID ADC49563 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 56
ID ADC47424 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 57
ID ADC44698 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 58
ID ADC47169 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 59
ID ADD08230 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 60
ID ADC82055 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003083461-A1.
PD 01-MAY-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 61
ID ADD07697 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 62
ID ADC78044 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 63
ID ADC82588 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003059833-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;

RESULT 64
ID ADD06279 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 65
ID ADD08768 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 66
ID ADC77798 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 67
ID ADD07017 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2002193100-A1.
PD 19-DEC-2002.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 68
ID ADC83264 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 69
ID ADD50761 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 70
ID ADD51007 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GENETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 71
ID ADD55371 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 72
ID ADD56329 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 73
ID ADD50488 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003096971-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 74
ID ADD54767 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 75
ID ADD50242 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 76
ID ADD51253 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 77
ID ADE26921 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 78
ID ADE26388 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 79
ID ADF67325 standard; cDNA; 907 BP.
DE Human PRO1187 nucleotide sequence SEQ ID NO:398.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 80
ID ADI35579 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003050457-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 81
ID ADI00072 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003045682-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 82
ID ABX77968 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #124.
PN US2003027163-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 83
ID ACD69286 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003100717-A1.
PD 29-MAY-2003.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 84
ID ABX90357 standard; cDNA; 907 BP.
DE Human secreted/transmembrane protein cDNA, #160.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 85
ID ACA66889 standard; cDNA; 907 BP.
DE cDNA encoding human PRO polypeptide #49.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 86
ID ACD66641 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 87
ID ABX64203 standard; cDNA; 907 BP.
DE cDNA encoding human PRO1187 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH) GENENTECH LTD.
Query Match 100.0%; Score 907; DB 10; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 88
ID ADC46800 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 89
ID ADE20971 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 90
ID ADE05815 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 91
ID ADD75044 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 92
ID ADD75790 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.


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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 93
ID ADD85022 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 94
ID ADD68848 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 95
ID ADE20725 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 96
ID ADE39022 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 97
ID ADE05569 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 98
ID ADD73554 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 99
ID ADD78394 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 100
ID ADE21217 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 101
ID ADD77332 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 102
ID ADE20479 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 103
ID ADD75544 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100654-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 104
ID ADD74060 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 105
ID ADD74306 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 106
ID ADD76036 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 107
ID ADD85528 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 108
ID ADE05077 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 109
ID ADD75290 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 110
ID ADD76834 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
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Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 111
ID ADD86602 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 112
ID ADD78070 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 113
ID ADD77578 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 114
ID ADD77824 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 115
ID ADD85282 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 116
ID ADD73814 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 117
ID ADD74552 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 118
ID ADD77080 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 119
ID ADD85774 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 120
ID AD805323 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 121
ID ADD74798 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 122
ID ADF35524 standard; cDNA; 907 BP.
DE cDNA encoding human PRO1187 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 123
ID ADG11774 standard; cDNA; 907 BP.
DE cDNA encoding human PRO1187 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 124
ID ADG05610 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 125
ID ADG27164 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 126
ID ADG11227 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 127
ID ADG12006 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 128
ID ADP94563 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 129
ID ADG06659 standard; cDNA; 907 BP.

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DE Human PRO polynucleotide #49.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 130
ID ADH19003 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 131
ID ADH19644 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003228656-A1.
PD 11-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 132
ID ADH21137 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003234358-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 133
ID ADH20177 standard; cDNA; 907 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1187.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 134
ID ADG34093 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 135
ID ADI33563 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 136
ID ADH69657 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 137
ID ADI29618 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 138
ID ADM27215 standard; cDNA; 907 BP.
DE Novel human secreted and transmembrane protein PRO1187 cDNA.
PN US2004044179-A1.

PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 139
ID ADK66573 standard; cDNA; 907 BP.
DE Human PRO polynucleotide #49.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 907; DB 12; Length 907;
Best Local Similarity 100.0%; Pred. No. 2.6e-250;
RESULT 140
ID ABK42709 standard; DNA; 17761 BP.
DE Genomic sequence #608 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 907; DB 4; Length 17761;
Best Local Similarity 100.0%; Pred. No. 8.3e-250;
RESULT 141
ID AAK79415 standard; DNA; 17761 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:34227.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 907; DB 4; Length 17761;
Best Local Similarity 100.0%; Pred. No. 8.3e-250;
RESULT 142
ID ADB60865 standard; DNA; 17761 BP.
DE Connective tissue related genomic DNA #608.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 100.0%; Score 907; DB 9; Length 17761;
Best Local Similarity 100.0%; Pred. No. 8.3e-250;
RESULT 143
ID ABZ11322 standard; cDNA; 1154 BP.
DE Human polynucleotide SEQ ID NO 204.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 66.3%; Score 601.6; DB 6; Length 1154;
Best Local Similarity 99.3%; Pred. No. 2e-162;
RESULT 144
ID ADM43840 standard; cDNA; 1154 BP.
DE Novel human arginine-rich protein cDNA #204.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANNC R T.
Query Match 66.3%; Score 601.6; DB 12; Length 1154;
Best Local Similarity 99.3%; Pred. No. 2e-162;
RESULT 145
ID AAF60563 standard; cDNA; 500 BP.
DE Receptor #51 partial coding sequence.
PN US6183968-B1.
PD 06-FEB-2001.
PA (INCYT) INCYTE PHARM INC.
Query Match 55.1%; Score 500; DB 4; Length 500;
Best Local Similarity 100.0%; Pred. No. 2.4e-133;
RESULT 146
ID ABL62546 standard; cDNA; 480 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:5524.
PN WO200192581-A2.
PD 06-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 50.5%; Score 458; DB 6; Length 480;
Best Local Similarity 99.6%; Pred. No. 2.9e-121;
RESULT 147
ID ABL80189 standard; cDNA; 425 BP.
DE Human ovarian cancer related cDNA clone SEQ ID NO:3167.

PN W0200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 44.4%; Score 403; DB 6; Length 425;
 Best Local Similarity 99.5%; Pred. No. 1.8e-105;
 RESULT 148
 ID ABL80621 standard; cDNA; 402 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:3599.
 PN W0200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 40.7%; Score 369; DB 6; Length 402;
 Best Local Similarity 99.3%; Pred. No. 1.1e-95;
 RESULT 149
 ID ABL8135 standard; cDNA; 360 BP.
 DE Human ovarian cancer related cDNA clone SEQ ID NO:6113.
 PN W0200192581-A2.
 PD 06-DEC-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 37.9%; Score 344.2; DB 6; Length 360;
 Best Local Similarity 98.9%; Pred. No. 1.4e-88;
 RESULT 150
 ID AAF66312 standard; cDNA; 399 BP.
 DE Novel human polynucleotide, SEQ ID NO: 2068.
 PN W0200102568-A2.
 PD 11-JAN-2001.
 PA (CHIR) CHIRON CORP.
 (HYSE-) HYSEQ INC.
 Query Match 24.6%; Score 222.8; DB 5; Length 399;
 Best Local Similarity 99.1%; Pred. No. 1.2e-53;
 RESULT 151
 ID AAF66311 standard; cDNA; 395 BP.
 DE Novel human polynucleotide, SEQ ID NO: 2067.
 PN W0200102568-A2.
 PD 11-JAN-2001.
 PA (CHIR) CHIRON CORP.
 (HYSE-) HYSEQ INC.
 Query Match 23.8%; Score 215.6; DB 5; Length 395;
 Best Local Similarity 98.2%; Pred. No. 1.4e-51;
 RESULT 152
 ID AAS35690 standard; DNA; 10093 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID No 1390.
 PN W0200155321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 213; DB 4; Length 10093;
 Best Local Similarity 85.8%; Pred. No. 2.7e-50;
 RESULT 153
 ID ABA07184 standard; DNA; 10093 BP.
 DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 503.
 PN W0200155206-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 213; DB 4; Length 10093;
 Best Local Similarity 85.8%; Pred. No. 2.7e-50;
 RESULT 154
 ID AAK89816 standard; DNA; 10093 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3392.
 PN W0200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 213; DB 4; Length 10093;
 Best Local Similarity 85.8%; Pred. No. 2.7e-50;
 RESULT 155
 ID ADB46584 standard; DNA; 10093 BP.
 DE Human cardiovascular system related genomic DNA #150.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 213; DB 10; Length 10093;
 Best Local Similarity 85.8%; Pred. No. 2.7e-50;
 RESULT 156
 ID ADJ08002 standard; DNA; 10093 BP.

DE Human cardiovascular system associated polypeptide-related DNA SegID1390.
 PN US2004005575-A1.
 PD 08-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 213; DB 13; Length 10093;
 Best Local Similarity 85.8%; Pred. No. 2.7e-50;
 RESULT 157
 ID AAL04218 standard; DNA; 32148 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6906.
 PN W0200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.5%; Score 212.8; DB 4; Length 32148;
 Best Local Similarity 83.8%; Pred. No. 4.8e-50;
 RESULT 158
 ID AAS36445 standard; DNA; 17397 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID No 1945.
 PN W0200155321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 10; Length 17397;
 Best Local Similarity 73.6%; Pred. No. 5.7e-50;
 RESULT 159
 ID ADB47139 standard; DNA; 17397 BP.
 DE Human cardiovascular system related genomic DNA #705.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 10; Length 17397;
 Best Local Similarity 73.6%; Pred. No. 5.7e-50;
 RESULT 160
 ID ADJ08557 standard; DNA; 17397 BP.
 DE Human cardiovascular system associated polypeptide-related DNA SegID1945.
 PN US2004005575-A1.
 PD 08-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 13; Length 17397;
 Best Local Similarity 73.6%; Pred. No. 5.7e-50;
 RESULT 161
 ID AAS36443 standard; DNA; 19334 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID No 1943.
 PN W0200155321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 4; Length 19334;
 Best Local Similarity 73.6%; Pred. No. 5.9e-50;
 RESULT 162
 ID ADB47137 standard; DNA; 19334 BP.
 DE Human cardiovascular system related genomic DNA #703.
 PN US2003059908-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 10; Length 19334;
 Best Local Similarity 73.6%; Pred. No. 5.9e-50;
 RESULT 163
 ID ADJ08555 standard; DNA; 19334 BP.
 DE Human cardiovascular system associated polypeptide-related DNA SegID1943.
 PN US2004005575-A1.
 PD 08-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 13; Length 19334;
 Best Local Similarity 73.6%; Pred. No. 5.9e-50;
 RESULT 164
 ID AAS36444 standard; DNA; 19345 BP.
 DE Human cardiovascular system antigen genomic DNA SEQ ID No 1944.
 PN W0200155321-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.4%; Score 212.2; DB 4; Length 19345;
 Best Local Similarity 73.6%; Pred. No. 5.9e-50;
 RESULT 165
 ID ADB47138 standard; DNA; 19345 BP.
 DE Human cardiovascular system related genomic DNA #704.

PN US2003059908-A1.
PD 27-MAR-2003.
Query Match (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity 23.4%; Score 212.2; DB 10; Length 19345;
RESULT 166
ID ADJ08556 standard; DNA; 19345 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID1944.
PN US2004005575-A1.
PD 08-JUN-2004.
Query Match (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity 23.4%; Score 212.2; DB 13; Length 19345;
RESULT 167
ID AD085575 standard; DNA; 29001 BP.
DE Human zinedin polynucleotide.
PN US2004110701-A1.
PD 10-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match
Best Local Similarity 73.6%; Score 212.2; DB 12; Length 29001;
RESULT 168
ID ACN44806 standard; DNA; 177587 BP.
DE Human genomic sequence hCG40093.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 23.4%; Score 211.8; DB 11; Length 177587;
RESULT 169
ID ACN44586 standard; DNA; 118931 BP.
DE Human genomic sequence hCG30014.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 23.3%; Score 211.6; DB 11; Length 118931;
RESULT 170
ID AAK91310 standard; DNA; 24664 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4886.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 23.3%; Score 211.2; DB 4; Length 24664;
RESULT 171
ID AAS32137 standard; DNA; 24664 BP.
DE Human liver associated genomic DNA #311.
PN WO200155355-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 23.3%; Score 211.2; DB 5; Length 24664;
RESULT 172
ID ABN90492 standard; DNA; 24664 BP.
DE Human liver antigen HPIV104 genomic sequence, SEQ ID NO: 613.
PN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match
Best Local Similarity 23.3%; Score 211.2; DB 6; Length 24664;
RESULT 173
ID ADJ15405 standard; DNA; 24664 BP.
DE Human liver-related genomic DNA - SEQ ID 613.
PN US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 23.3%; Score 211.2; DB 11; Length 24664;
RESULT 174
ID ADP13332 standard; DNA; 126990 BP.

DE Renal cell carcinoma differentially expressed gene #68.
PN WO2004048933-A2.
PD 10-JUN-2004.
PA (AMHP) WYETH.
PA (TWIN/) TWINE N C.
PA (BURC/) BURCZYNSKI M E.
PA (TREB/) TREPICCHIO W L.
PA (DORN/) DORNER A.
PA (STOV/) STOVER J A.
PA (SLON/) SLONI D K.
Query Match
Best Local Similarity 23.2%; Score 210.6; DB 12; Length 126990;
RESULT 175
ID ADH59595 standard; DNA; 301 BP.
DE Alu-repeat consensus sequence #1.
PN WO2003027328-A2.
PD 03-APR-2003.
PA (BOST-) BOSTON PROBES INC.
PA (DAKO-) DAKOCYTOMATION DENMARK AS.
Query Match
Best Local Similarity 23.2%; Score 210; DB 10; Length 301;
RESULT 176
ID AAK79904 standard; DNA; 2744 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34716.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 23.1%; Score 209.8; DB 4; Length 2744;
RESULT 177
ID AAF97846 standard; DNA; 51474 BP.
DE Human neuroblastoma cell line NB-1 ip36 nucleotide sequence SEQ ID NO:60.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREPCTURE.
Query Match
Best Local Similarity 23.1%; Score 209.8; DB 5; Length 51474;
RESULT 178
ID ABR83569 standard; cDNA; 122888 BP.
DE Human cDNA differentially expressed in granulocytic cells #140.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match
Best Local Similarity 23.1%; Score 209.8; DB 6; Length 122888;
RESULT 179
ID AAL36855 standard; DNA; 19616 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3220.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 23.1%; Score 209.4; DB 4; Length 19616;
RESULT 180
ID ABA16856 standard; DNA; 19616 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9187.
PN WO200155063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 23.1%; Score 209.4; DB 5; Length 19616;
RESULT 181
ID ABA16094 standard; DNA; 19616 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8425.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 23.1%; Score 209.4; DB 5; Length 19616;
RESULT 182
ID ABX59843 standard; cDNA; 19616 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2187.

PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 23.1%; Score 209.4; DB 8; Length 19616;
 Best Local Similarity 86.7%; Pred. No. 3.8e-49;
 RESULT 183
 ID ADJ30593 standard; DNA; 19616 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3220.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.4; DB 12; Length 19616;
 Best Local Similarity 86.7%; Pred. No. 3.8e-49;
 RESULT 184
 ID AAI62651 standard; DNA; 614 BP.
 DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 301.
 PN WO200155324-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 614;
 Best Local Similarity 83.3%; Pred. No. 1.1e-49;
 RESULT 185
 ID AAI06745 standard; DNA; 614 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9433.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 614;
 Best Local Similarity 83.3%; Pred. No. 1.1e-49;
 RESULT 186
 ID AAI62649 standard; DNA; 691 BP.
 DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 299.
 PN WO200155324-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 691;
 Best Local Similarity 83.3%; Pred. No. 1.2e-49;
 RESULT 187
 ID AAI06743 standard; DNA; 691 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9431.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 691;
 Best Local Similarity 83.3%; Pred. No. 1.2e-49;
 RESULT 188
 ID AAI62650 standard; DNA; 16225 BP.
 DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 300.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 189
 ID AAK81913 standard; DNA; 16225 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 36725.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 190
 ID AAI06744 standard; DNA; 16225 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9432.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 4; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 191
 ID AAS30106 standard; DNA; 16225 BP.

DE Human lung antigen genomic DNA #176.
 PN WO200155303-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 5; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 192
 ID ADB33443 standard; DNA; 16225 BP.
 DE Human novel lung related polypeptide DNA SEQ ID NO 370.
 PN US2003054368-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 23.1%; Score 209.2; DB 10; Length 16225;
 Best Local Similarity 83.3%; Pred. No. 4e-49;
 RESULT 193
 ID ADA43380 standard; cDNA; 50000 BP.
 DE Human aethma associated gene, AAGB, genomic fragment #1.
 PN US2003104521-A1.
 PD 05-JUN-2003.
 PA (WHIT/) WHITTAKER P A.
 Query Match 23.1%; Score 209.2; DB 6; Length 50000;
 Best Local Similarity 82.5%; Pred. No. 6.2e-49;
 RESULT 194
 ID ABA98944 standard; DNA; 50000 BP.
 DE Human aethma-associated gene AAGB genomic DNA #1.
 PN WO200206312-A2.
 PD 24-JAN-2002.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 Query Match 23.1%; Score 209.2; DB 6; Length 50000;
 Best Local Similarity 82.5%; Pred. No. 6.2e-49;
 RESULT 195
 ID ABL42416 standard; DNA; 59065 BP.
 DE Human serine/threonine kinase DNA.
 PN US6340583-B1.
 PD 22-JAN-2002.
 PA (PEKE) PE CORP NY.
 Query Match 23.1%; Score 209.2; DB 6; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 196
 ID AAD41839 standard; DNA; 59065 BP.
 DE Human LIM domain kinase (LIMK) gene.
 PN US6403353-B1.
 PD 11-JUN-2002.
 PA (PEKE) PE CORP NY.
 Query Match 23.1%; Score 209.2; DB 6; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 197
 ID ADG98727 standard; DNA; 59065 BP.
 DE Human kinase genomic DNA.
 PN US2003166215-A1.
 PD 04-SEP-2003.
 PA (PEKE) PE CORP NY.
 Query Match 23.1%; Score 209.2; DB 10; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 198
 ID ADR44808 standard; DNA; 59065 BP.
 DE Human kinase genomic DNA.
 PN US2004175751-A1.
 PD 09-SEP-2004.
 PA (APPL) APPLERA CORP.
 Query Match 23.1%; Score 209.2; DB 13; Length 59065;
 Best Local Similarity 79.7%; Pred. No. 6.6e-49;
 RESULT 199
 ID ABK63459 standard; cDNA; 128978 BP.
 DE Human cDNA differentially expressed in granulocytic cells #30.
 PN WO200228899-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 23.1%; Score 209.2; DB 6; Length 128978;
 Best Local Similarity 79.7%; Pred. No. 9e-49;
 RESULT 200
 ID AAD54587 standard; DNA; 128978 BP.

DE Human LTM kinase (LINK) DNA #6.
PN WO200299048-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 23.1%; Score 209.2; DB 8; Length 128978;
Best Local Similarity 79.7%; Pred. No. 9e-49;
RESULT 201
ID ADR52994 standard; DNA; 128978 BP.
DE Drug therapy altered expressed gene #345.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP) MYETH.
PA (BURE/) BURCZYNSKI M.
PA (TWIN/) TWINE N. J.
PA (DORN/) DORNER A. J.
PA (TREE/) TREPTICHO W. L.
Query Match 23.1%; Score 209.2; DB 13; Length 128978;
Best Local Similarity 79.7%; Pred. No. 9e-49;
RESULT 202
Query Match 23.0%; Score 209; DB 11; Length 110000;
Best Local Similarity 84.4%; Pred. No. 9.6e-49;
RESULT 203
ID ADQ18757 standard; DNA; 43712 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1576.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 23.0%; Score 208.8; DB 12; Length 43712;
Best Local Similarity 82.7%; Pred. No. 7.7e-49;
RESULT 204
ID ADQ97727 standard; DNA; 73063 BP.
DE Human cancer associated sequence HD10-034, SEQ ID 704.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 23.0%; Score 208.8; DB 12; Length 73063;
Best Local Similarity 85.1%; Pred. No. 9.4e-49;
RESULT 205
ID ABR42912 standard; DNA; 518 BP.
DE Genomic sequence #811 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 208.6; DB 4; Length 518;
Best Local Similarity 83.6%; Pred. No. 1.6e-49;
RESULT 206
ID ADB61068 standard; DNA; 518 BP.
DE Connective tissue related genomic DNA #811.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 208.6; DB 9; Length 518;
Best Local Similarity 83.6%; Pred. No. 1.6e-49;
RESULT 207
ID ADE82948 standard; DNA; 167163 BP.
DE Human PVTI genomic DNA sequence.
PN WO2003060808-A2.
PD 02-OCT-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 23.0%; Score 208.6; DB 10; Length 167163;
Best Local Similarity 84.6%; Pred. No. 1.5e-48;
RESULT 208
ID AAK79905 standard; DNA; 2744 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34717.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 23.0%; Score 208.2; DB 4; Length 2744;
Best Local Similarity 82.3%; Pred. No. 4e-49;
RESULT 209
ID ADN06353 standard; DNA; 398800 BP.
DE Human FLAP genomic DNA SEQ ID NO:1.
PN WO2004035741-A2.

PD 29-APR-2004.
PA (DECO-) DECODE GENETICS EHF.
Query Match 23.0%; Score 208.2; DB 12; Length 110000;
Best Local Similarity 82.3%; Pred. No. 1.6e-48;
RESULT 210
ID ADS94372 standard; DNA; 398800 BP.
DE Human 5-lipoxygenase activating protein (FLAP) gene.
PN WO2004035746-A2.
PD 29-APR-2004.
PA (DECO-) DECODE GENETICS EHF.
Query Match 23.0%; Score 208.2; DB 13; Length 110000;
Best Local Similarity 82.3%; Pred. No. 1.6e-48;
RESULT 211
ID ABL69793 standard; DNA; 291 BP.
DE Prostate cancer related gene sequence SEQ ID NO:8130.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 22.9%; Score 208; DB 6; Length 291;
Best Local Similarity 87.2%; Pred. No. 1.9e-49;
RESULT 212
ID ABL67475 standard; DNA; 291 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5812.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 22.9%; Score 208; DB 6; Length 291;
Best Local Similarity 87.2%; Pred. No. 1.9e-49;
RESULT 213
ID ADP65796 standard; DNA; 270150 BP.
DE Human 16P13 sequence section 7 of 8 DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 22.9%; Score 208; DB 11; Length 270150;
Best Local Similarity 79.2%; Pred. No. 2.6e-48;
RESULT 214
ID AAK71190 standard; DNA; 3139 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26002.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.9%; Score 207.8; DB 4; Length 3139;
Best Local Similarity 78.7%; Pred. No. 5.4e-49;
RESULT 215
ID ADQ20461 standard; DNA; 166181 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3281.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.9%; Score 207.8; DB 12; Length 166181;
Best Local Similarity 85.0%; Pred. No. 2.5e-48;
RESULT 216
ID ADQ18633 standard; DNA; 166181 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1452.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.9%; Score 207.8; DB 12; Length 166181;
Best Local Similarity 85.0%; Pred. No. 2.5e-48;
RESULT 217
ID AAD27781 standard; DNA; 31766 BP.
DE Human sulphate transporter protein splice form genomic DNA.
PN WO200181412-A2.
PD 01-NOV-2001.
PA (PEKE) PE CORP NY.
Query Match 22.9%; Score 207.6; DB 6; Length 31766;
Best Local Similarity 85.8%; Pred. No. 1.5e-48;
RESULT 218
ID AAL50687 standard; DNA; 31766 BP.
DE Human sulphate transporter protein genomic DNA sequence.
PN WO200259306-A2.
PD 01-AUG-2002.

PA (APPL-) APPLERA CORP. 22.9%; Score 207.6; DB 6; Length 31766;
Query Match
Best Local Similarity 85.8%; Pred. No. 1.5e-48;
RESULT 219
ID ABR84242 standard; cDNA; 43599 BP.
DE Human cDNA differentially expressed in granulocytic cells #813.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.9%; Score 207.4; DB 6; Length 43599;
Best Local Similarity 84.0%; Pred. No. 1.9e-48;
RESULT 220
ID ADE11169 standard; DNA; 394191 BP.
DE Human transporter protein encoding gene SEQ ID NO:1.
Query Match 22.8%; Score 207.2; DB 10; Length 110000;
Best Local Similarity 86.3%; Pred. No. 3.2e-48;
RESULT 221
ID ABA16169 standard; DNA; 4969 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8500.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.8%; Score 207; DB 5; Length 4969;
Best Local Similarity 84.2%; Pred. No. 1.1e-48;
RESULT 222
ID ABR83502 standard; cDNA; 77425 BP.
DE Human cDNA differentially expressed in granulocytic cells #73.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.8%; Score 206.8; DB 6; Length 77425;
Best Local Similarity 86.3%; Pred. No. 3.6e-48;
RESULT 223
ID ADQ59434 standard; DNA; 169659 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:70.
PN WO200405828-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.8%; Score 206.8; DB 12; Length 169659;
Best Local Similarity 79.4%; Pred. No. 4.9e-48;
RESULT 224
ID ADQ97721 standard; DNA; 178024 BP.
DE Human cancer associated sequence HD10-033, SEQ ID 698.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.8%; Score 206.6; DB 12; Length 178024;
Best Local Similarity 82.0%; Pred. No. 5.7e-48;
RESULT 225
ID ADQ02756 standard; DNA; 96594 BP.
DE Human MOPR carcinoma associated gene, SEQ ID NO:1274.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.8%; Score 206.4; DB 9; Length 96594;
Best Local Similarity 84.0%; Pred. No. 5.1e-48;
RESULT 226
ID ADB72494 standard; DNA; 96594 BP.
DE Human MOPR gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.8%; Score 206.4; DB 10; Length 96594;
Best Local Similarity 84.0%; Pred. No. 5.1e-48;
RESULT 227
ID ADC85236 standard; DNA; 96594 BP.
DE Human MOPR genomic sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.8%; Score 206.4; DB 10; Length 96594;
Best Local Similarity 84.0%; Pred. No. 5.1e-48;
RESULT 228
ID ADM74351 standard; DNA; 96594 BP.
DE Human carcinoma associated (CA) nucleic acid #10.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39341.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 4; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 230
ID ADA98945 standard; DNA; 16146 BP.
DE Human secreted protein-related DNA sequence #538.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 8; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 231
ID ADA44551 standard; DNA; 16146 BP.
DE Human secreted protein DNA SEQ ID 744.
PN WO2003000865-A2.
PD 03-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 8; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 232
ID ADC20980 standard; DNA; 16146 BP.
DE Human secreted protein-related DNA sequence #398.
PN WO200292787-A2.
PD 21-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 10; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 233
ID ADP11004 standard; DNA; 16146 BP.
DE Human secreted protein encoding sequence #326.
PN WO200299085-A2.
PD 12-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 10; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 234
ID ABR17011 standard; DNA; 16146 BP.
DE Human secreted protein-related DNA sequence - SEQ ID NO 365.
PN WO2002077188-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 10; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 235
ID ABR68089 standard; DNA; 16146 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1612.
PN WO2002077186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 206.2; DB 10; Length 16146;
Best Local Similarity 82.2%; Pred. No. 2.9e-48;
RESULT 236
ID ACN44482 standard; DNA; 34096 BP.
DE Human genomic sequence hCG26017.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.7%; Score 206.2; DB 11; Length 34096;
Best Local Similarity 78.4%; Pred. No. 3.9e-48;
RESULT 237

ID AAF58067 standard; DNA; 39198 BP.
DE Human polyamine-modulated factor-1 PMF-1 gene.
PN WO200107610-A1.
PD 01-FEB-2001.
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 22.7%; Score 206.2; DB 5; Length 39198;
Best Local Similarity 84.7%; Pred. No. 4.1e-48;
RESULT 238
ID ABB89533 standard; DNA; 48436 BP.
DE Human corneal N-acetylglucosamine-6-sulfotransferase DNA SEQ ID NO:38.
PN US2002061562-A1.
PD 23-MAY-2002.
PA (FUKU/) FUKUDA M N.
Query Match 22.7%; Score 206.2; DB 6; Length 48436;
Best Local Similarity 79.9%; Pred. No. 4.5e-48;
RESULT 239
ID ADL13501 standard; DNA; 167932 BP.
DE Osteoarthritis-associated polymorphic nucleotide #33.
PN WO200305416-A2.
PD 03-JUL-2003.
PA (INCYT) INCYTE GENOMICS INC.
Query Match 22.7%; Score 206.2; DB 10; Length 167932;
Best Local Similarity 84.7%; Pred. No. 7.2e-48;
RESULT 240
ID ABB87883 standard; DNA; 50849 BP.
DE Human glutathione reductase (GSR) gene SEQ ID NO:1.
PN WO200242320-A2.
PD 30-MAY-2002.
PA (GENA-) GENMISANCE PHARM INC.
Query Match 22.7%; Score 206; DB 6; Length 50849;
Best Local Similarity 81.7%; Pred. No. 5.2e-48;
RESULT 241
ID ADQ97152 standard; DNA; 58651 BP.
DE Human cancer associated sequence HD08-008, SEQ ID NO:128.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.7%; Score 206; DB 12; Length 58651;
Best Local Similarity 79.0%; Pred. No. 5.5e-48;
RESULT 242
ID ABA16120 standard; DNA; 447 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8451.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.8; DB 5; Length 447;
Best Local Similarity 84.9%; Pred. No. 9.6e-49;
RESULT 244
ID ABA20765 standard; DNA; 447 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13096.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.8; DB 5; Length 447;
Best Local Similarity 84.9%; Pred. No. 9.6e-49;
RESULT 245
ID AAK6925 standard; DNA; 451 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:22737.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.8; DB 4; Length 451;
Best Local Similarity 84.9%; Pred. No. 9.7e-49;
RESULT 246
ID AAK81748 standard; DNA; 451 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36560.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.7%; Score 205.8; DB 4; Length 451;
Best Local Similarity 84.9%; Pred. No. 9.7e-49;
RESULT 247
ID ABA16121 standard; DNA; 451 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8452.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.7%; Score 205.8; DB 5; Length 451;
Best Local Similarity 84.9%; Pred. No. 9.7e-49;
RESULT 248
ID AAG92779 standard; DNA; 6905 BP.
DE Human rhymopoietin continuous gene fragment.
PN WO9517205-A1.
PD 29-JUN-1995.
PA (IMMU-) IMMUNOBIOLOGY RES INST INC.
Query Match 22.7%; Score 205.8; DB 2; Length 6905;
Best Local Similarity 83.6%; Pred. No. 2.8e-48;
RESULT 249
ID ADO19382 standard; DNA; 6905 BP.
DE Human PRO polynucleotide #720.
PN WO200404361-A2.
PD 27-MAY-2004.
PA (GENT) GENENTECH INC.
Query Match 22.7%; Score 205.8; DB 12; Length 6905;
Best Local Similarity 83.6%; Pred. No. 2.8e-48;
RESULT 250
ID ACN37228 standard; DNA; 32640 BP.
DE Human periodontal disease related gene KRT23 SEQ ID NO:138.
PN WO2004042054-A1.
PD 21-MAY-2004.
PA (HUBI-) HUBIT GENOMIX INC.
Query Match 22.7%; Score 205.8; DB 13; Length 32640;
Best Local Similarity 82.4%; Pred. No. 5e-48;
RESULT 251
ID ACN43878 standard; DNA; 39148 BP.
DE Human genomic sequence hCG36720.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.7%; Score 205.8; DB 11; Length 39148;
Best Local Similarity 83.6%; Pred. No. 5.4e-48;
RESULT 252
ID ADA02696 standard; DNA; 59554 BP.
DE Human TK2 carcinoma associated gene, SEQ ID NO:1214.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.7%; Score 205.8; DB 9; Length 59554;
Best Local Similarity 86.3%; Pred. No. 6.3e-48;
RESULT 253
ID ADB72434 standard; DNA; 59554 BP.
DE Human TK2 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.7%; Score 205.8; DB 10; Length 59554;
Best Local Similarity 86.3%; Pred. No. 6.3e-48;
RESULT 254
ID ADB95944 standard; DNA; 59554 BP.
DE Human TK2 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.7%; Score 205.8; DB 10; Length 59554;
Best Local Similarity 86.3%; Pred. No. 6.3e-48;
RESULT 255
ID ABA16034 standard; DNA; 203654 BP.
DE Human gene encoding calcium channel transporter family member.
PN US2002142938-A1.
PD 03-OCT-2002.
PA (YANC/) YAN C.

PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match
Best Local Similarity 22.7%; Score 205.8; DB 10; Length 203654;
RESULT 256
ID AAS42054 standard; DNA; 10085 BP.
DE Genomic sequence #370 encoding novel human enzyme polypeptide.
PN W0200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 22.7%; Score 205.6; DB 4; Length 10085;
RESULT 257
ID AAL02803 standard; DNA; 10085 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5491.
PN W0200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 22.7%; Score 205.6; DB 4; Length 10085;
RESULT 258
ID AAD5634 standard; DNA; 142519 BP.
DE Human chromodomain helicase DNA binding protein (CHD) encoding DNA #9.
PN W0200298899-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 22.7%; Score 205.6; DB 10; Length 142519;
RESULT 259
ID AAS23041 standard; DNA; 719 BP.
DE DNA encoding novel bone marrow polypeptide #135.
PN W0200157187-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 4; Length 719;
RESULT 260
ID ABO72698 standard; cDNA; 2619 BP.
DE Human MDR1 encoding cDNA SEQ ID NO 250.
PN W0200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 6; Length 2619;
RESULT 261
ID AAK84729 standard; DNA; 48037 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39541.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 4; Length 48037;
RESULT 262
ID AAK85983 standard; DNA; 48037 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40795.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 4; Length 48037;
RESULT 263
ID AAK84730 standard; DNA; 48045 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39542.
PN W0200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 4; Length 48045;
RESULT 264
ID AAK85984 standard; DNA; 48045 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40796.
PN W0200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 4; Length 48045;
RESULT 265
ID AAZ00870 standard; DNA; 56516 BP.
DE PGI genomic coding sequence.
PN W0932644-A2.
PD 01-JUL-1999.
PA (GEST-) GENSET.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 2; Length 56516;
RESULT 266
ID AAZ01022 standard; DNA; 56520 BP.
DE Wild type PGI coding sequence.
PN W0932644-A2.
PD 01-JUL-1999.
PA (GEST-) GENSET.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 2; Length 56520;
RESULT 267
ID ADC85367 standard; DNA; 96593 BP.
DE Mouse Bim coding sequence.
PN W02003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 10; Length 96593;
RESULT 268
ID ADA02888 standard; DNA; 96594 BP.
DE Human BLM carcinoma associated gene, SEQ ID NO:1406.
PN W02003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 9; Length 96594;
RESULT 269
ID ADB72626 standard; DNA; 96594 BP.
DE Human BLM gene.
PN W02003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 10; Length 96594;
RESULT 270
ID ADM74483 standard; DNA; 96594 BP.
DE Human carcinoma associated (CA) nucleic acid #76.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MOKR/) MORRIS D W.
PA (ENGE/) ENGELHARD E K.
Query Match
Best Local Similarity 22.6%; Score 205.4; DB 12; Length 96594;
RESULT 271
ID ADH59596 standard; DNA; 301 BP.
DE Ali-repeat consensus sequence #2.
PN W02003027328-A2.
PD 03-APR-2003.
PA (BOST-) BOSTON PROBES INC.
PA (DAKO-) DAKOCYTOMATION DENMARK AS.
Query Match
Best Local Similarity 22.6%; Score 205.2; DB 10; Length 301;
RESULT 272
ID AAL52585 standard; cDNA; 3673 BP.
DE Human BHD mutant truncated cDNA SEQ ID NO: 3.
PN W02003102149-A2.
PD 11-DEC-2003.
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 22.6%; Score 205.2; DB 12; Length 3673;
RESULT 273
ID AAL52588 standard; cDNA; 3673 BP.
DE Human BHD mutant truncated cDNA SEQ ID NO: 9.

PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3673;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 274
ID AAL52584 standard; cDNA; 3674 BP.
DE Human BHD coding sequence.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3674;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 275
ID AAL52589 standard; cDNA; 3674 BP.
DE Human BHD mutant truncated cDNA SEQ ID NO: 11.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3674;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 276
ID AAL52587 standard; cDNA; 3675 BP.
DE Human BHD mutant truncated cDNA SEQ ID NO: 7.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3675;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 277
ID AAL52618 standard; DNA; 3676 BP.
DE Human BHD consensus sequence.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3676;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 278
ID AAL52586 standard; cDNA; 3702 BP.
DE Human BHD mutant truncated cDNA SEQ ID NO: 5.
PN WO2003102149-A2.
PD 11-DEC-2003.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.6%; Score 205.2; DB 12; Length 3702;
Best Local Similarity 81.2%; Pred. No. 3.2e-48;
RESULT 279
ID AAK80061 standard; DNA; 5279 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34873.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.2; DB 4; Length 5279;
Best Local Similarity 83.4%; Pred. No. 3.7e-48;
RESULT 280
ID AAK80062 standard; DNA; 5279 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34874.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.2; DB 4; Length 5279;
Best Local Similarity 83.4%; Pred. No. 3.7e-48;
RESULT 281
ID AAK80060 standard; DNA; 5279 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34872.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 205.2; DB 4; Length 5279;
Best Local Similarity 83.4%; Pred. No. 3.7e-48;
RESULT 282
ID AAZ60888 standard; DNA; 17131 BP.
DE DNA encoding a human geranylgeranyl pyrophosphate synthetase (hGGPPS).
PN WO200005382-A2.

PD 03-FEB-2000.
PA (GEST) GENSET.
Query Match 22.6%; Score 205.2; DB 3; Length 17131;
Best Local Similarity 83.3%; Pred. No. 5.8e-48;
RESULT 283
ID AAA35185 standard; DNA; 32351 BP.
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:59.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.6%; Score 205.2; DB 3; Length 32351;
Best Local Similarity 77.8%; Pred. No. 7.5e-48;
RESULT 284
ID AAP21307 standard; DNA; 32351 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2874.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.6%; Score 205.2; DB 3; Length 32351;
Best Local Similarity 77.8%; Pred. No. 7.5e-48;
RESULT 285
ID AB297001 standard; DNA; 32351 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.6%; Score 205.2; DB 10; Length 32351;
Best Local Similarity 77.8%; Pred. No. 7.5e-48;
RESULT 286
ID ABD20850 standard; DNA; 32351 BP.
DE Human pulmonary and inflammatory target DNA #461.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.6%; Score 205.2; DB 11; Length 32351;
Best Local Similarity 77.8%; Pred. No. 7.5e-48;
RESULT 287
ID AAA35189 standard; DNA; 40298 BP.
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:63.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.6%; Score 205.2; DB 3; Length 40298;
Best Local Similarity 77.8%; Pred. No. 8.1e-48;
RESULT 288
ID AAF21311 standard; DNA; 40298 BP.
DE Human low adenosine antisense oligonucleotide related sequence #2878.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.6%; Score 205.2; DB 3; Length 40298;
Best Local Similarity 77.8%; Pred. No. 8.1e-48;
RESULT 289
ID AB297005 standard; DNA; 40298 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.6%; Score 205.2; DB 10; Length 40298;
Best Local Similarity 77.8%; Pred. No. 8.1e-48;
RESULT 290
ID ABD20854 standard; DNA; 40298 BP.
DE Human pulmonary and inflammatory target DNA #465.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.6%; Score 205.2; DB 11; Length 40298;
Best Local Similarity 77.8%; Pred. No. 8.1e-48;
RESULT 291
ID ADJ10262 standard; DNA; 51001 BP.
DE Human geranylgeranyl diphosphate synthase 1 genomic DNA Segid 11.

PN US2004005570-A1.
PD 08-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 22.6%; Score 205.2; DB 12; Length 51001;
Best Local Similarity 83.3%; Pred. No. 8.9e-48;
RESULT 292
ID ADL13556 standard; DNA; 95240 BP.
DE Osteoarthritis-associated polymorphic nucleotide #88.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.6%; Score 205.2; DB 10; Length 95240;
Best Local Similarity 84.7%; Pred. No. 1.1e-47;
RESULT 293
ID ABK93497 standard; CDNA; 227968 BP.
DE Human cDNA differentially expressed in granulocytic cells #68.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.6%; Score 205; DB 6; Length 227968;
Best Local Similarity 84.1%; Pred. No. 1.8e-47;
RESULT 294
ID ADQ18538 standard; DNA; 227968 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1357.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.6%; Score 205; DB 12; Length 227968;
Best Local Similarity 84.1%; Pred. No. 1.8e-47;
RESULT 295
ID AAQ923781 standard; DNA; 3234 BP.
DE Human thymopolein gene fragment.
PN WO9517205-A1.
PD 29-JUN-1995.
PA (IMMU-) IMMUNOBIOLOGY RES. INST INC.
Query Match 22.6%; Score 204.8; DB 2; Length 3234;
Best Local Similarity 76.5%; Pred. No. 4e-48;
RESULT 296
ID AAS41738 standard; DNA; 32217 BP.
DE Genomic sequence #54 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 204.8; DB 4; Length 32217;
Best Local Similarity 79.6%; Pred. No. 9.7e-48;
RESULT 297
ID ADJ10262 standard; DNA; 51001 BP.
DE Human geranylgeranyl diphosphate synthase 1 genomic DNA SeqID 11.
PN US2004005570-A1.
PD 08-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 22.6%; Score 204.8; DB 12; Length 51001;
Best Local Similarity 77.1%; Pred. No. 1.2e-47;
RESULT 298
ID ADC87336 standard; DNA; 108316 BP.
DE Human GPCR gene SEQ ID NO:1789.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
DE (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATOR.
Query Match 22.6%; Score 204.8; DB 10; Length 108316;
Best Local Similarity 81.2%; Pred. No. 1.5e-47;
RESULT 299
Query Match 22.6%; Score 204.8; DB 12; Length 110000;
Best Local Similarity 73.1%; Pred. No. 1.6e-47;
RESULT 300
ID AAK86146 standard; DNA; 16997 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40958.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 204.6; DB 4; Length 16997;
Best Local Similarity 81.8%; Pred. No. 8.7e-48;

RESULT 301
ID AAK80033 standard; DNA; 16997 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34845.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.6%; Score 204.6; DB 4; Length 16997;
Best Local Similarity 81.8%; Pred. No. 8.7e-48;
RESULT 302
ID ACN44998 standard; DNA; 122614 BP.
DE Human genomic sequence hCG29191.
PN WO2003073825-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.6%; Score 204.6; DB 11; Length 122614;
Best Local Similarity 83.2%; Pred. No. 1.9e-47;
RESULT 303
ID ADL08109 standard; DNA; 247682 BP.
DE Human gene associated with low HDL-C AT3.
PN US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 22.6%; Score 204.6; DB 12; Length 247682;
Best Local Similarity 81.8%; Pred. No. 2.4e-47;
RESULT 304
ID AAK85292 standard; DNA; 2680 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40104.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 2680;
Best Local Similarity 82.7%; Pred. No. 4.9e-48;
RESULT 305
ID AAL45661 standard; DNA; 5970 BP.
DE Mammary gland bioreactor related DNA #2.
PN CN1324952-A.
PD 05-DEC-2001.
PA (ZHON-) ZHONGLU BIOLOGICAL ENG CO LTD SHANGHAI.
Query Match 22.5%; Score 204.4; DB 6; Length 5970;
Best Local Similarity 81.4%; Pred. No. 6.6e-48;
RESULT 306
ID AAA34833 standard; DNA; 6870 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2522.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.5%; Score 204.4; DB 3; Length 6870;
Best Local Similarity 81.4%; Pred. No. 7e-48;
RESULT 307
ID AAP20955 standard; DNA; 6870 BP.
DE Interleukin-11 polynucleotide fragment #2522.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.5%; Score 204.4; DB 3; Length 6870;
Best Local Similarity 81.4%; Pred. No. 7e-48;
RESULT 308
ID ABZ96649 standard; DNA; 6870 BP.
DE Human interleukin-11 nucleic acid.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.5%; Score 204.4; DB 10; Length 6870;
Best Local Similarity 81.4%; Pred. No. 7e-48;
RESULT 309
ID ABD19514 standard; DNA; 6870 BP.
DE Human interleukin-11 DNA fragment #3.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.5%; Score 204.4; DB 11; Length 6870;
Best Local Similarity 81.4%; Pred. No. 7e-48;

RESULT 310
ID AAA34834 standard; DNA; 8055 BP.
DE Human adenosine receptor related polynucleotide SEQ ID NO:2523.
PN WO200009525-A2.
PD 24-FEB-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.5%; Score 204.4; DB 3; Length 8055;
Best Local Similarity 81.4%; Pred. No. 7.4e-48;
RESULT 311
ID AAF20956 standard; DNA; 8055 BP.
DE Interleukin-11 polynucleotide fragment #2523.
PN WO200062736-A2.
PD 26-OCT-2000.
PA (UYEC-) UNIV EAST CAROLINA.
Query Match 22.5%; Score 204.4; DB 3; Length 8055;
Best Local Similarity 81.4%; Pred. No. 7.4e-48;
RESULT 312
ID ABZ9650 standard; DNA; 8055 BP.
DE Human nucleic acid sequence.
PN WO200285308-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.5%; Score 204.4; DB 10; Length 8055;
Best Local Similarity 81.4%; Pred. No. 7.4e-48;
RESULT 313
ID ABD19512 standard; DNA; 8055 BP.
DE Human Interleukin-11 DNA fragment #1.
PN WO200285309-A2.
PD 31-OCT-2002.
PA (EPIC-) EPIGENESIS PHARM INC.
Query Match 22.5%; Score 204.4; DB 11; Length 8055;
Best Local Similarity 81.4%; Pred. No. 7.4e-48;
RESULT 314
ID AAK87584 standard; DNA; 14417 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42396.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 315
ID AAK71816 standard; DNA; 14417 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26628.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 316
ID AAK71113 standard; DNA; 14417 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27925.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 317
ID AAI62923 standard; DNA; 14417 BP.
DE Human genomic DNA SEQ ID NO 251.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 318
ID ABZ74674 standard; DNA; 14417 BP.
DE Secreted protein gene 391 genomic fragment HB8FC45, SEQ ID NO:1821.
PN WO20027013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 8; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;

RESULT 319
ID ABZ68196 standard; DNA; 14417 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1719.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 10; Length 14417;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 320
ID AAK73099 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27911.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 321
ID AAK87568 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42380.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 322
ID AAK85290 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40102.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 323
ID AAK71814 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26626.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 324
ID AAI62921 standard; DNA; 14426 BP.
DE Human genomic DNA SEQ ID NO 249.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 4; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 325
ID ABZ74673 standard; DNA; 14426 BP.
DE Secreted protein gene 391 genomic fragment HB8FC45, SEQ ID NO:1820.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 8; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 326
ID ABZ68195 standard; DNA; 14426 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1718.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.5%; Score 204.4; DB 10; Length 14426;
Best Local Similarity 82.7%; Pred. No. 9.3e-48;
RESULT 327
ID ABD32665 standard; DNA; 112453 BP.
DE Human cancer-associated genomic DNA HD13-070.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.5%; Score 204.4; DB 13; Length 112453;
Best Local Similarity 83.9%; Pred. No. 2e-47;
RESULT 328

ID ADQ59167 standard; DNA; 120670 BP.
 DE MSI-H carcinoma genomic DNA sequence SEQ ID NO:4.
 PN KR2004008012-A.
 PD 28-JAN-2004.
 PA (KIMH/) KIM H G.
 DE (KIMH/) KIM H G.
 PA (LEEJ/) LEE J S.
 PA (RHEB/) RHEB H S.
 Query Match
 Best Local Similarity 22.5%; Score 204.4; DB 12; Length 120670;
 ID ADE82948 standard; DNA; 167163 BP.
 DE Human PVT1 genomic DNA sequence.
 PN WO2003080808-A2.
 PD 02-OCT-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match
 Best Local Similarity 22.5%; Score 204.4; DB 10; Length 167163;
 ID AAF21437 standard; DNA; 209273 BP.
 DE Human factor-related antisense polynucleotide #3004.
 PN WO200062736-A2.
 PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 Query Match
 Best Local Similarity 22.5%; Score 204.4; DB 3; Length 209273;
 ID ABZ97131 standard; DNA; 209274 BP.
 DE Human enzyme-related antisense polynucleotide.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIC-) EPIGENESIS PHARM INC.
 Query Match
 Best Local Similarity 22.5%; Score 204.4; DB 10; Length 209274;
 ID ABD17970 standard; DNA; 209284 BP.
 DE Human factor-related antisense polynucleotide.
 PN WO200285309-A2.
 PD 31-OCT-2002.
 PA (EPIC-) EPIGENESIS PHARM INC.
 Query Match
 Best Local Similarity 22.5%; Score 204.4; DB 11; Length 209284;
 ID ABA96807 standard; CDNA; 1777 BP.
 DE Human uteroglobin 9-encoding cDNA.
 PN WO200198337-A1.
 PD 27-DEC-2001.
 PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
 Query Match
 Best Local Similarity 22.5%; Score 204.2; DB 6; Length 1777;
 ID AAC69133 standard; DNA; 4736 BP.
 DE Human ABC1 gene exon 2.
 PN WO200055318-A2.
 PD 21-SEP-2000.
 PA (UYBR-) UNIV BRITISH COLUMBIA.
 PA (XENO-) XENON BIOSRESEARCH INC.
 Query Match
 Best Local Similarity 22.5%; Score 204.2; DB 3; Length 4736;
 ID AAS04033 standard; DNA; 11754 BP.
 DE Human ABC1 gene, partial genomic clone #1.
 PN WO200130848-A2.
 PD 03-MAY-2001.
 PA (AVET-) AVENTIS PHARMA SA.
 Query Match
 Best Local Similarity 22.5%; Score 204.2; DB 4; Length 11754;
 ID ABL58149 standard; DNA; 11754 BP.
 DE Human ABCA1 transporter gene fragment #3.
 PN WO200236770-A2.
 PD 10-MAY-2002.
 PA (AVET-) AVENTIS PHARMA SA.
 Query Match
 Best Local Similarity 22.5%; Score 204.2; DB 6; Length 11754;
 ID ABL97677 standard; DNA; 22927 BP.
 DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2329.
 PN WO200155317-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 22.5%; Score 204; DB 4; Length 22927;
 ID ADC86460 standard; DNA; 33137 BP.
 DE Human GPCR gene SEQ ID NO:913.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NRAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match
 Best Local Similarity 22.5%; Score 204; DB 10; Length 33137;
 ID ACH03435 standard; DNA; 48840 BP.
 DE Genomic DNA encoding human latrophilin 1 (LPH1).
 PN US2003054347-A1.
 PD 20-MAR-2003.
 PA (UNMI-) UNIV MICHIGAN.
 Query Match
 Best Local Similarity 22.5%; Score 204; DB 9; Length 48840;
 ID ABR48904 standard; DNA; 3635 BP.
 DE Novel human kallikrein KLK15, Intron 1.
 PN WO200214485-A2.
 PD 21-FEB-2002.
 PA (MOUN-) MOUNT SINAI HOSPITAL.
 Query Match
 Best Local Similarity 22.5%; Score 203.8; DB 6; Length 3635;
 ID ABR48346 standard; DNA; 8735 BP.
 DE Genomic DNA encoding novel human kallikrein KLK15.
 PN WO200214485-A2.
 PD 21-FEB-2002.
 PA (MOUN-) MOUNT SINAI HOSPITAL.
 Query Match
 Best Local Similarity 22.5%; Score 203.8; DB 6; Length 8735;
 ID ADN10936 standard; DNA; 8735 BP.
 DE Human kallikrein 15 gene, marker of endocrine cancer.

PN WO2004029285-A2.
PD 08-APR-2004.
PA (MOUN) MOUNT SINAI HOSPITAL.
Query Match 22.5%; Score 203.8; DB 13; Length 8735;
Best Local Similarity 86.2%; Pred. No. 1.1e-47;
RESULT 346
ID ADS36456 standard; DNA; 16640 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1670.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.5%; Score 203.8; DB 13; Length 16640;
Best Local Similarity 86.2%; Pred. No. 1.5e-47;
RESULT 347
ID ADS36479 standard; DNA; 18235 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1693.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.5%; Score 203.8; DB 13; Length 18235;
Best Local Similarity 86.2%; Pred. No. 1.5e-47;
RESULT 348
ID ADA02714 standard; DNA; 53413 BP.
DE Human VDAC1 carcinoma associated gene, SEQ ID NO:1232.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.5%; Score 203.8; DB 9; Length 53413;
Best Local Similarity 79.5%; Pred. No. 2.3e-47;
RESULT 349
ID ADB72452 standard; DNA; 53413 BP.
DE Human VDAC1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.5%; Score 203.8; DB 10; Length 53413;
Best Local Similarity 79.5%; Pred. No. 2.3e-47;
RESULT 350
ID ADB95962 standard; DNA; 53413 BP.
DE Human VDAC1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.5%; Score 203.8; DB 10; Length 53413;
Best Local Similarity 79.5%; Pred. No. 2.3e-47;
RESULT 351
ID AAD41740 standard; DNA; 99500 BP.
DE Human RECQL2 DNA #1.
PN US6399378-B1.
PD 04-JUN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 22.5%; Score 203.8; DB 6; Length 99500;
Best Local Similarity 83.6%; Pred. No. 2.9e-47;
RESULT 352
ID ADL13728 standard; DNA; 151212 BP.
DE Osteoarthritis-associated polymorphic nucleotide #260.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.5%; Score 203.8; DB 10; Length 151212;
Best Local Similarity 78.9%; Pred. No. 3.4e-47;
RESULT 353
ID AAK7082 standard; DNA; 4658 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:41894.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.6; DB 4; Length 4658;
Best Local Similarity 82.8%; Pred. No. 1e-47;
RESULT 354
ID ABZ73865 standard; DNA; 18902 BP.
DE Secreted protein gene 71 genomic fragment HCRBF72, SEQ ID NO:1012.
PN WO200277013-A2.

PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.6; DB 8; Length 18902;
Best Local Similarity 81.6%; Pred. No. 1.7e-47;
RESULT 355
ID ABZ67444 standard; DNA; 18902 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 967.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.6; DB 10; Length 18902;
Best Local Similarity 81.6%; Pred. No. 1.7e-47;
RESULT 356
ID ADD71350 standard; DNA; 93390 BP.
DE Glutamine:fructose-6-phosphate amide transferase 1 genomic sequence.
PN WO2003023063-A1.
PD 20-MAR-2003.
PA (SANY) SANKYO CO LTD.
Query Match 22.4%; Score 203.6; DB 10; Length 93390;
Best Local Similarity 79.8%; Pred. No. 3.2e-47;
RESULT 357
ID AAK77913 standard; DNA; 644 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:32725.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 644;
Best Local Similarity 83.7%; Pred. No. 5.4e-48;
RESULT 358
ID AAK77915 standard; DNA; 646 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:32727.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 646;
Best Local Similarity 83.7%; Pred. No. 5.4e-48;
RESULT 359
ID AAI64724 standard; cDNA; 777 BP.
DE Human polynucleotide SEQ ID NO 4784.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSECO INC.
Query Match 22.4%; Score 203.4; DB 4; Length 777;
Best Local Similarity 79.7%; Pred. No. 5.8e-48;
RESULT 360
ID ACN39520 standard; cDNA; 2068 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325729, SEQ ID NO:3715.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GENTH) GENTENTECH INC.
Query Match 22.4%; Score 203.4; DB 13; Length 2068;
Best Local Similarity 81.3%; Pred. No. 8.5e-48;
RESULT 361
ID AAK77914 standard; DNA; 2558 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:32726.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 2558;
Best Local Similarity 83.7%; Pred. No. 9.2e-48;
RESULT 362
ID AAL04534 standard; DNA; 4067 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7222.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 4067;
Best Local Similarity 79.1%; Pred. No. 1.1e-47;
RESULT 363
ID AAL04537 standard; DNA; 4067 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7225.
PN WO200155320-A2.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 4067;
Best Local Similarity 79.1%; Pred. No. 1.1e-47;
RESULT 364
ID ABL97457 standard; DNA; 4067 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2109.
PD WO200155317-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 4067;
Best Local Similarity 79.1%; Pred. No. 1.1e-47;
RESULT 365
ID ABL97460 standard; DNA; 4067 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2112.
PD WO200155317-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 4067;
Best Local Similarity 79.1%; Pred. No. 1.1e-47;
RESULT 366
ID AAK77916 standard; DNA; 7759 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:32728.
PD WO200157182-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 7759;
Best Local Similarity 83.7%; Pred. No. 1.4e-47;
RESULT 367
ID AAK73223 standard; DNA; 31051 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28035.
PD WO200157182-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 31051;
Best Local Similarity 77.9%; Pred. No. 2.4e-47;
RESULT 368
ID AAK89112 standard; DNA; 32190 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2688.
PD WO200155314-A2.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 4; Length 32190;
Best Local Similarity 83.7%; Pred. No. 2.4e-47;
RESULT 369
ID AAS31862 standard; DNA; 32190 BP.
DE Human liver associated genomic DNA #36.
PD WO200155355-A1.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 5; Length 32190;
Best Local Similarity 83.7%; Pred. No. 2.4e-47;
RESULT 370
ID ABR90217 standard; DNA; 32190 BP.
DE Human liver antigen HPLS161 genomic sequence, SEQ ID NO:338.
PD US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.4%; Score 203.4; DB 6; Length 32190;
Best Local Similarity 83.7%; Pred. No. 2.4e-47;
RESULT 371
ID ADJ15130 standard; DNA; 32190 BP.
DE Human liver-related genomic DNA - SEQ ID 338.
PD US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.4; DB 11; Length 32190;
Best Local Similarity 83.7%; Pred. No. 2.4e-47;
RESULT 372
ID ABB69695 standard; DNA; 56737 BP.
DE Human hypoxanthine-guanine phosphoribosyltransferase (HPRRT) gene.
PD US2002102731-A1.

PD 01-AUG-2002.
PA (UYNY) UNIV NEW YORK STATE RES FOUND.
Query Match 22.4%; Score 203.4; DB 6; Length 56737;
Best Local Similarity 83.8%; Pred. No. 3e-47;
RESULT 373
ID ADL08126 standard; DNA; 191395 BP.
DE Human gene associated with low HDL-C PA12.
PD US2004043389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 22.4%; Score 203.4; DB 12; Length 191395;
Best Local Similarity 83.8%; Pred. No. 4.9e-47;
RESULT 374
ID ABD32868 standard; DNA; 238417 BP.
DE Human cancer-associated genomic DNA HD17-053.
PD WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.4%; Score 203.4; DB 13; Length 238417;
Best Local Similarity 83.8%; Pred. No. 5.3e-47;
RESULT 375
ID ABV74806 standard; cDNA; 2009 BP.
DE Signalase 11.22 coding sequence.
PD CN1345931-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BLOWNDOW GENE DEV INC.
Query Match 22.4%; Score 203.2; DB 6; Length 2009;
Best Local Similarity 83.0%; Pred. No. 9.6e-48;
RESULT 376
ID AAF97867 standard; DNA; 13161 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:81.
PD WO200116311-A1.
PD 08-MAR-2001.
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 22.4%; Score 203.2; DB 5; Length 13161;
Best Local Similarity 83.3%; Pred. No. 2e-47;
RESULT 377
ID AAK78275 standard; DNA; 35959 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33087.
PD WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203.2; DB 4; Length 35959;
Best Local Similarity 78.7%; Pred. No. 2.9e-47;
RESULT 378
ID ADL13850 standard; DNA; 180550 BP.
DE Osteoarthritis-associated polymorphic nucleotide #382.
PD WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.4%; Score 203.2; DB 10; Length 180550;
Best Local Similarity 81.8%; Pred. No. 5.4e-47;
RESULT 379
ID ACN44398 standard; DNA; 194883 BP.
DE Human genomic sequence hCG20056.
PD WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.4%; Score 203.2; DB 11; Length 194883;
Best Local Similarity 75.1%; Pred. No. 5.6e-47;
RESULT 380
ID ABD33276 standard; DNA; 256190 BP.
DE Human cancer-associated (CA) gene HD07-048.
PD WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.4%; Score 203.2; DB 13; Length 256190;
Best Local Similarity 83.3%; Pred. No. 6.2e-47;
RESULT 381
ID AAK80969 standard; DNA; 6187 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35781.
PD WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 203; DB 4; Length 6187;
Best Local Similarity 81.7%; Pred. No. 1.7e-47;
RESULT 382
ID ABLN96931 standard; DNA; 99014 BP.
DE Gene #1429 used to diagnose liver cancer.
PN WO200228103-A2.
PD 11-APR-2002.
PA (HUMA-) GENE LOGIC INC.
Query Match 22.4%; Score 203; DB 6; Length 99014;
Best Local Similarity 76.4%; Pred. No. 4.9e-47;
RESULT 383
ID AAD08215 standard; DNA; 114793 BP.
DE Human genome from BAC clone, hbm168.
PN WO200142434-A1.
PD 14-JUN-2001.
PA (MER) MERCK & CO INC.
Query Match 22.4%; Score 203; DB 4; Length 114793;
Best Local Similarity 84.1%; Pred. No. 5.2e-47;
RESULT 384
ID ACN44170 standard; DNA; 196686 BP.
DE Human genomic sequence hCG39530.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.4%; Score 203; DB 11; Length 196686;
Best Local Similarity 83.7%; Pred. No. 6.4e-47;
RESULT 385
ID ADQ97523 standard; DNA; 215974 BP.
DE Human cancer associated sequence HD09-008, SEQ ID 500.
PN WO2004060304-A2.
PD 22-UTL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.4%; Score 203; DB 12; Length 215974;
Best Local Similarity 81.7%; Pred. No. 6.6e-47;
RESULT 386
ID AAD04910 standard; cDNA; 2013 BP.
DE Human secreted protein-encoding gene 4 cDNA clone HSLH186, SEQ ID NO:23.
PN WO200134799-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 2013;
Best Local Similarity 74.0%; Pred. No. 1.3e-47;
RESULT 387
ID AAL04936 standard; DNA; 3753 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7624.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 3753;
Best Local Similarity 79.2%; Pred. No. 1.6e-47;
RESULT 388
ID ABL97830 standard; DNA; 3753 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2482.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 3753;
Best Local Similarity 79.2%; Pred. No. 1.6e-47;
RESULT 389
ID AAD04901 standard; cDNA; 3781 BP.
DE Human secreted protein-encoding gene 4 cDNA clone HSLH186, SEQ ID NO:14.
PN WO200134799-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 3781;
Best Local Similarity 74.0%; Pred. No. 1.6e-47;
RESULT 390
ID AAK71815 standard; DNA; 14448 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26627.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14448;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 391
ID AAK87580 standard; DNA; 14448 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42392.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14448;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 392
ID AAK73111 standard; DNA; 14448 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27923.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14448;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 393
ID AAI62922 standard; DNA; 14448 BP.
DE Human genomic DNA SEQ ID NO 250.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14448;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 394
ID AAK73116 standard; DNA; 14451 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27928.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14451;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 395
ID AAK71818 standard; DNA; 14451 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26630.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14451;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 396
ID AAK87587 standard; DNA; 14451 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42399.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14451;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 397
ID AAI62925 standard; DNA; 14451 BP.
DE Human genomic DNA SEQ ID NO 253.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 14451;
Best Local Similarity 82.4%; Pred. No. 2.7e-47;
RESULT 398
ID AAL03917 standard; DNA; 22299 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6605.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.4%; Score 202.8; DB 4; Length 22299;
Best Local Similarity 83.6%; Pred. No. 3.2e-47;
RESULT 399
ID AAS40317 standard; DNA; 22299 BP.
DE Human encoding human prostate cancer antigen, Seq ID No 469.
PN WO200155316-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.4%; Score 202.8; DB 5; Length 22299;
 Best Local Similarity 83.6%; Pred. No. 3.2e-47;
 RESULT 400
 ID ADJ09523 standard; DNA; 22299 BP.
 DE Human prostate cancer associated gene-related DNA SeqID469.
 PN US2003054373-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.4%; Score 202.8; DB 11; Length 22299;
 Best Local Similarity 83.6%; Pred. No. 3.2e-47;
 RESULT 401
 ID ADM97421 standard; DNA; 26865 BP.
 DE Prostate and breast cancer associated human gene CYP17.
 PN WO2004028346-A2.
 PD 08-APR-2004.
 PA (AMSH) AMERSHAM BIOSCIENCES SV CORP.
 Query Match 22.4%; Score 202.8; DB 12; Length 26865;
 Best Local Similarity 78.9%; Pred. No. 3.4e-47;
 RESULT 402
 ID AAD50021 standard; DNA; 27067 BP.
 DE Human secreted protein encoding gene.
 Query Match 22.4%; Score 202.8; DB 10; Length 27067;
 Best Local Similarity 83.6%; Pred. No. 3.4e-47;
 RESULT 403
 ID AAA35003 standard; DNA; 56583 BP.
 DE Human adenocarcinoma receptor related polynucleotide SEQ ID NO:2692.
 PN WO200009525-A2.
 PD 24-FEB-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 22.4%; Score 202.8; DB 3; Length 56583;
 Best Local Similarity 83.4%; Pred. No. 4.5e-47;
 RESULT 404
 ID AAF21125 standard; DNA; 56583 BP.
 DE Human low adenocarcinoma antileukemia oligonucleotide related sequence #2692.
 PN WO2000062736-A2.
 PD 26-OCT-2000.
 PA (UYEC-) UNIV EAST CAROLINA.
 Query Match 22.4%; Score 202.8; DB 3; Length 56583;
 Best Local Similarity 83.4%; Pred. No. 4.5e-47;
 RESULT 405
 ID AB296819 standard; DNA; 56583 BP.
 DE Human nucleic acid sequence.
 PN WO200285308-A2.
 PD 31-OCT-2002.
 PA (EPIC-) EPIDERMIS PHARM INC.
 Query Match 22.4%; Score 202.8; DB 10; Length 56583;
 Best Local Similarity 83.4%; Pred. No. 4.5e-47;
 RESULT 406
 ID ABD20668 standard; DNA; 56583 BP.
 DE Human pulmonary and inflammatory target DNA #279.
 PN WO200285309-A2.
 PD 31-OCT-2002.
 PA (EPIC-) EPIDERMIS PHARM INC.
 Query Match 22.4%; Score 202.8; DB 11; Length 56583;
 Best Local Similarity 83.4%; Pred. No. 4.5e-47;
 RESULT 407
 ID ACN44066 standard; DNA; 99886 BP.
 DE Human genomic sequence hCG15674.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.4%; Score 202.8; DB 11; Length 99886;
 Best Local Similarity 79.2%; Pred. No. 5.6e-47;
 RESULT 408
 ID ADQ17329 standard; DNA; 101685 BP.
 DE Human bovine tissue sarcoma-upregulated DNA - SEQ ID 146.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 22.4%; Score 202.8; DB 12; Length 101685;
 Best Local Similarity 79.2%; Pred. No. 5.7e-47;
 RESULT 409

ID ACN45054 standard; DNA; 133632 BP.
 DE Human genomic sequence hCG28560.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.4%; Score 202.8; DB 11; Length 133632;
 Best Local Similarity 76.0%; Pred. No. 6.3e-47;
 RESULT 410
 ID ADC56769 standard; DNA; 1051 BP.
 DE DNA (SeqID 4) related to the human thymidylate acid synthetase gene.
 PN JP2003102480-A.
 PD 08-APR-2003.
 PA (SRLS-) SRL KK.
 Query Match 22.3%; Score 202.6; DB 10; Length 1051;
 Best Local Similarity 81.7%; Pred. No. 1.1e-47;
 RESULT 411
 ID AAS34702 standard; DNA; 3147 BP.
 DE Human DNA for a novel foetal antigen, SEQ ID NO 2126.
 PN WO200155312-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202.6; DB 5; Length 3147;
 Best Local Similarity 83.1%; Pred. No. 1.7e-47;
 RESULT 412
 ID AAF5338 standard; cDNA; 3200 BP.
 DE Human TGF-beta receptor cDNA clone HDKX45.
 PN WO200112670-A1.
 PD 22-FEB-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.3%; Score 202.6; DB 4; Length 3200;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 413
 ID ABR14000 standard; cDNA; 3353 BP.
 DE cDNA encoding human protein kinase 3700.
 PN WO20024921-A2.
 PD 28-MAR-2002.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 22.3%; Score 202.6; DB 6; Length 3353;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 414
 ID ADL14160 standard; cDNA; 3353 BP.
 DE Novel human gene 3700 cDNA.
 PN US2004058355-A1.
 PD 25-MAR-2004.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 22.3%; Score 202.6; DB 12; Length 3353;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 415
 ID AAD26459 standard; cDNA; 3360 BP.
 DE Human kinase PKIN-12 cDNA.
 PN WO200196547-A2.
 PD 20-DEC-2001.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 22.3%; Score 202.6; DB 6; Length 3360;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 416
 ID AAK94280 standard; cDNA; 3395 BP.
 DE Human full-length cDNA, SEQ ID NO: 2918.
 PN EP133094-A2.
 PD 05-SEP-2001.
 PA (HELT-) HELIX RES INST.
 Query Match 22.3%; Score 202.6; DB 4; Length 3395;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 417
 ID ADL30885 standard; cDNA; 3395 BP.
 DE Full length human cDNA clone SeqID 2918.
 PN EP1339543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 22.3%; Score 202.6; DB 12; Length 3395;
 Best Local Similarity 81.7%; Pred. No. 1.7e-47;
 RESULT 418
 ID ABX71420 standard; cDNA; 3443 BP.

DE Human cell cycle-associated cDNA from clone DKFzphes3_7j3.
PN WO200112659-A2.
PD 22-FEB-2001.
PA (GENU-) GERMAN HUMAN GENOME PROJECT.
Query Match 22.3%; Score 202.6; DB 5; Length 3443;
Best Local Similarity 81.7%; Pred. No. 1.8e-47;
RESULT 419
ID ADF79664 standard; cDNA; 3443 BP.
DE Novel human secreted and transmembrane protein cDNA SeqID 639.
PN WO200307203-A2.
PD 04-SEP-2003.
PA (GETH-) GENENTECH INC.
Query Match 22.3%; Score 202.6; DB 10; Length 3443;
Best Local Similarity 81.7%; Pred. No. 1.8e-47;
RESULT 420
ID ADF81952 standard; DNA; 3443 BP.
DE Leukemia-related DNA sequence #2508.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFB/) HAFERLACH T.
PA (SCHO/) SCHUCH C.
PA (KERN/) KERN W.
Query Match 22.3%; Score 202.6; DB 10; Length 3443;
Best Local Similarity 81.7%; Pred. No. 1.8e-47;
RESULT 421
ID ADO20171 standard; cDNA; 3443 BP.
DE Human PRO polynucleotide #540.
PN WO2004043361-A2.
PD 27-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 22.3%; Score 202.6; DB 12; Length 3443;
Best Local Similarity 81.7%; Pred. No. 1.8e-47;
RESULT 422
ID AAK6979 standard; DNA; 4646 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23791.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 4; Length 4646;
Best Local Similarity 82.3%; Pred. No. 2e-47;
RESULT 423
ID ABA20357 standard; DNA; 11585 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12688.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 5; Length 11585;
Best Local Similarity 83.3%; Pred. No. 2.8e-47;
RESULT 424
ID AAS36927 standard; DNA; 20869 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 2427.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 4; Length 20869;
Best Local Similarity 85.6%; Pred. No. 3.5e-47;
RESULT 425
ID AAK85001 standard; DNA; 20869 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39813.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 4; Length 20869;
Best Local Similarity 85.6%; Pred. No. 3.5e-47;
RESULT 426
ID ABA16245 standard; DNA; 20869 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8576.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 5; Length 20869;
Best Local Similarity 85.6%; Pred. No. 3.5e-47;
RESULT 427
ID ADE47621 standard; DNA; 20869 BP.
DE Human cardiovascular system related genomic DNA #1187.
PN US2003059908-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 10; Length 20869;
Best Local Similarity 85.6%; Pred. No. 3.5e-47;
RESULT 428
ID ADJ09039 standard; DNA; 20869 BP.
DE Human cardiovascular system associated polypeptide-related DNA SeqID2427.
PN US2004005575-A1.
PD 08-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 13; Length 20869;
Best Local Similarity 85.6%; Pred. No. 3.5e-47;
RESULT 429
ID AAK82338 standard; DNA; 48908 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37150.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.6; DB 4; Length 48908;
Best Local Similarity 81.7%; Pred. No. 4.9e-47;
RESULT 430
ID AAK6125 standard; DNA; 556 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20937.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 556;
Best Local Similarity 82.6%; Pred. No. 1e-47;
RESULT 431
ID AAK6126 standard; DNA; 556 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20938.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 556;
Best Local Similarity 82.6%; Pred. No. 1e-47;
RESULT 432
ID AAS36105 standard; DNA; 32195 BP.
DE Human cardiovascular system antigen genomic DNA SEQ ID NO 1605.
PN WO200155321-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 433
ID AAS31538 standard; DNA; 32195 BP.
DE Human DNA for a novel extracellular matrix protein, Seq ID No 617.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 434
ID AAS31532 standard; DNA; 32195 BP.
DE Human DNA for a novel extracellular matrix protein, Seq ID No 611.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;
RESULT 435
ID ABA4045 standard; DNA; 32195 BP.
DE Genomic DNA encoding novel central nervous system protein #260.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202.4; DB 4; Length 32195;
Best Local Similarity 79.9%; Pred. No. 4.8e-47;

RESULT 436
 ID ABQ6862 standard; DNA; 32195 BP.
 DE Human polynucleotide seq ID NO 611.
 PN US2002042386-A1.
 PD 11-APR-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 6; Length 32195;
 79.9%; Pred. No. 4.8e-47;
 RESULT 437
 ID ABQ6862 standard; DNA; 32195 BP.
 DE Human polynucleotide seq ID NO 617.
 PN US2002042386-A1.
 PD 11-APR-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 6; Length 32195;
 79.9%; Pred. No. 4.8e-47;
 RESULT 438
 ID ADC1143 standard; DNA; 32195 BP.
 DE Human DNA from extracellular matrix gene 112 #1.
 PN US2003059875-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 10; Length 32195;
 79.9%; Pred. No. 4.8e-47;
 RESULT 439
 ID ADC1149 standard; DNA; 32195 BP.
 DE Human DNA from extracellular matrix gene 113 #1.
 PN US2003059875-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 10; Length 32195;
 79.9%; Pred. No. 4.8e-47;
 RESULT 440
 ID ADE4679 standard; DNA; 32195 BP.
 DE Human cardiovascular system related genomic DNA #365.
 PN US2003059875-A1.
 PD 27-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 10; Length 32195;
 79.9%; Pred. No. 4.8e-47;
 RESULT 441
 ID ADI5503 standard; DNA; 32195 BP.
 DE Novel human protein genomic DNA seq id 1233.
 PN US2004018969-A1.
 PD 29-JAN-2004.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 12; Length 32195;
 79.9%; Pred. No. 4.8e-47;
 RESULT 442
 ID ADJ08217 standard; DNA; 32195 BP.
 DE Human cardiovascular system associated polypeptide-related DNA SeqID1605.
 PN US2004005575-A1.
 PD 08-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 13; Length 32195;
 79.9%; Pred. No. 4.8e-47;
 RESULT 443
 ID ACN37205 standard; DNA; 34079 BP.
 DE Human periodontal disease related gene COL18A1 SEQ ID NO.115.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 13; Length 34079;
 81.2%; Pred. No. 4.9e-47;
 RESULT 444
 ID AAK83781 standard; DNA; 37664 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO.38593.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 4; Length 37664;
 81.2%; Pred. No. 5e-47;
 RESULT 445
 ID ADQ18757 standard; DNA; 43712 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1576.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 12; Length 43712;
 77.6%; Pred. No. 5.3e-47;
 RESULT 446
 ID AAK83782 standard; DNA; 61710 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO.38594.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.2; DB 4; Length 61710;
 81.2%; Pred. No. 6.1e-47;
 RESULT 447
 ID AAL57580 standard; cDNA; 93273 BP.
 DE Human GTPase activating protein-like cDNA.
 PN WO2003059148-A2.
 PD 24-JUL-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 9; Length 93273;
 79.9%; Pred. No. 7.2e-47;
 RESULT 448
 ID ABD32827 standard; DNA; 129381 BP.
 DE Human cancer-associated genomic DNA HD17-008.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.4; DB 13; Length 129381;
 81.2%; Pred. No. 8.1e-47;
 RESULT 449
 ID AAZ50359 standard; DNA; 9365 BP.
 DE Human CD39-L4 genomic DNA.
 PN WO200004041-A2.
 PD 27-JAN-2000.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.2; DB 3; Length 9365;
 78.6%; Pred. No. 3.4e-47;
 RESULT 450
 ID AAF63405 standard; DNA; 9365 BP.
 DE Human CD39 like protein CD39-L4 partial DNA sequence.
 PN WO200110205-A1.
 PD 15-FEB-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.2; DB 4; Length 9365;
 78.6%; Pred. No. 3.4e-47;
 RESULT 451
 ID AAF63406 standard; DNA; 14747 BP.
 DE Human CD39 like protein CD39-L4 genomic DNA sequence.
 PN WO200110205-A1.
 PD 15-FEB-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.2; DB 4; Length 14747;
 78.6%; Pred. No. 4e-47;
 RESULT 452
 ID AAF63407 standard; DNA; 15977 BP.
 DE Human CD39 like protein CD39-L4 genomic DNA sequence #2.
 PN WO200110205-A1.
 PD 15-FEB-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 22.3%; Score 202.2; DB 4; Length 15977;
 78.6%; Pred. No. 4.1e-47;
 RESULT 453
 ID ACN44382 standard; DNA; 30558 BP.
 DE Human genomic sequence hCG15773.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.

Query Match 22.3%; Score 202.2; DB 11; Length 30558;
Best Local Similarity 85.8%; Pred. No. 5.3e-47;
ID ABRN96931 standard; DNA; 99014 BP.
DE Gene #3429 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.3%; Score 202.2; DB 6; Length 99014;
Best Local Similarity 79.5%; Pred. No. 8.4e-47;
RESULT 455
ID ACN43994 standard; DNA; 109586 BP.
DE Human genomic sequence hCG23847.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGE-) SAGES DISCOVERY.
Query Match 22.3%; Score 202.2; DB 11; Length 109586;
Best Local Similarity 83.2%; Pred. No. 8.7e-47;
RESULT 456
ID ADP03055 standard; cDNA; 124987 BP.
DE Human housekeeping gene cDNA #96.
PN JF200413552-A.
PD 13-MAY-2004.
PA (NIG) NGK INSULATORS LTD.
Query Match 22.3%; Score 202.2; DB 12; Length 124987;
Best Local Similarity 82.1%; Pred. No. 9.1e-47;
RESULT 457
ID ADS88553 standard; cDNA; 124990 BP.
DE Human housekeeping gene cDNA sequence SEQ ID NO:96.
PN WO2004035785-A1.
PD 29-APR-2004.
PA (NIG) NGK INSULATORS LTD.
Query Match 22.3%; Score 202.2; DB 13; Length 124990;
Best Local Similarity 82.1%; Pred. No. 9.1e-47;
RESULT 458
ID ACH25975 standard; cDNA; 502 BP.
DE Human adult ovary cDNA #3355.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 22.3%; Score 202; DB 9; Length 502;
Best Local Similarity 72.7%; Pred. No. 1.2e-47;
RESULT 459
ID ADD19251 standard; cDNA; 843 BP.
DE Human cDNA from secreted protein gene 68.
PN WO2003052377-A2.
PD 26-JUN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 843;
Best Local Similarity 81.5%; Pred. No. 1.5e-47;
RESULT 460
ID ADD19217 standard; cDNA; 878 BP.
DE Human cDNA from secreted protein gene 34.
PN WO2003052377-A2.
PD 26-JUN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 878;
Best Local Similarity 81.5%; Pred. No. 1.5e-47;
RESULT 461
ID ADM2980 standard; cDNA; 1960 BP.
DE Human cDNA of the invention SEQ ID NO:1665.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (RES-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.3%; Score 202; DB 11; Length 1960;
Best Local Similarity 78.2%; Pred. No. 2.1e-47;
RESULT 462
ID ADD18777 standard; DNA; 8672 BP.
DE Human disease related protein DNA sequence SeqID208.

PN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 22.3%; Score 202; DB 10; Length 8672;
Best Local Similarity 74.6%; Pred. No. 3.7e-47;
RESULT 463
ID AAK72319 standard; DNA; 15090 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27131.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 4; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 464
ID ABR69842 standard; DNA; 15090 BP.
DE Human secreted protein gene 22 genomic DNA fragment #3.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 6; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 465
ID ABR69843 standard; DNA; 15090 BP.
DE Human secreted protein gene 22 genomic DNA fragment #4.
PN WO200226931-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 6; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 466
ID ACC50857 standard; cDNA; 15090 BP.
DE Human secreted protein BAC clone SEQ ID NO 1037.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 8; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 467
ID ACC50858 standard; cDNA; 15090 BP.
DE Human secreted protein BAC clone SEQ ID NO 1038.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 8; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 468
ID ABR71480 standard; DNA; 15090 BP.
DE Secreted protein gene 12 genomic fragment HAUAI83, SEQ ID NO:590.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 8; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 469
ID ABR71479 standard; DNA; 15090 BP.
DE Secreted protein gene 12 genomic fragment HAUAI83, SEQ ID NO:589.
PN WO200276488-A1.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 8; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 470
ID ADB91835 standard; DNA; 15090 BP.
DE Human secreted protein related DNA #SEQ ID 781.
PN WO2003004622-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 9; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 471
ID ADB91836 standard; DNA; 15090 BP.
DE Human secreted protein related DNA #SEQ ID 782.
PN WO2003004622-A2.

PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 9; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 472
ID ADCT4610 standard; DNA; 15090 BP.
DE Human secreted protein-related DNA - SEQ ID 1243.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 473
ID ADC74611 standard; DNA; 15090 BP.
DE Human secreted protein-related DNA - SEQ ID 1244.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 474
ID ADD38131 standard; cDNA; 15090 BP.
DE CDNA clone in ATCC deposit #25.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 475
ID ADD38130 standard; cDNA; 15090 BP.
DE CDNA clone in ATCC deposit #24.
PN WO200290526-A2.
PD 14-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 476
ID ADA57724 standard; DNA; 15090 BP.
DE BAC fragment containing human secreted protein gene #302.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 477
ID ADA57725 standard; DNA; 15090 BP.
DE BAC fragment containing human secreted protein gene #302.
PN WO2002102994-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.3%; Score 202; DB 10; Length 15090;
Best Local Similarity 83.0%; Pred. No. 4.6e-47;
RESULT 478
ID ADA02630 standard; DNA; 32433 BP.
DE Human FLT3 carcinoma associated gene, SEQ ID NO:1148.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.3%; Score 202; DB 9; Length 32433;
Best Local Similarity 80.3%; Pred. No. 6.2e-47;
RESULT 479
ID ADB72368 standard; DNA; 32433 BP.
DE Human FLT3 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.3%; Score 202; DB 10; Length 32433;
Best Local Similarity 80.3%; Pred. No. 6.2e-47;
RESULT 480
ID ADB95678 standard; DNA; 32433 BP.
DE Human FLT3 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.3%; Score 202; DB 10; Length 32433;
Best Local Similarity 80.3%; Pred. No. 6.2e-47;
RESULT 481
ID ABD33115 standard; DNA; 69652 BP.
DE Human cancer-associated (CA) gene HD07-011.
PN WO2004058146-A2.
PD 15-UTL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.3%; Score 202; DB 13; Length 69652;
Best Local Similarity 77.1%; Pred. No. 8.3e-47;
RESULT 482
ID ABD32868 standard; DNA; 238417 BP.
DE Human cancer-associated genomic DNA HD17-053.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.3%; Score 202; DB 13; Length 238417;
Best Local Similarity 82.8%; Pred. No. 1.3e-46;
RESULT 483
ID AAK79410 standard; DNA; 4883 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34222.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 4; Length 4883;
Best Local Similarity 78.1%; Pred. No. 3.4e-47;
RESULT 484
ID ADQ64434 standard; cDNA; 8331 BP.
DE Novel human cDNA sequence #1595.
PN RP1440981-A2.
PD 28-UTL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.2%; Score 201.8; DB 12; Length 8331;
Best Local Similarity 83.5%; Pred. No. 4.2e-47;
RESULT 485
ID AAS33461 standard; DNA; 9192 BP.
DE DNA encoding human secreted protein, Seq ID No 744.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 4; Length 9192;
Best Local Similarity 81.0%; Pred. No. 4.4e-47;
RESULT 486
ID AAL36577 standard; DNA; 11991 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2942.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 4; Length 11991;
Best Local Similarity 76.9%; Pred. No. 4.8e-47;
RESULT 487
ID AAL07205 standard; DNA; 11991 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9893.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 4; Length 11991;
Best Local Similarity 76.9%; Pred. No. 4.8e-47;
RESULT 488
ID AAX59565 standard; cDNA; 11991 BP.
DE CDNA encoding novel human musculoskeletal system antigen #1909.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBS/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.2%; Score 201.8; DB 8; Length 11991;
Best Local Similarity 76.9%; Pred. No. 4.8e-47;
RESULT 489
ID ADJ30315 standard; DNA; 11991 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2942.
PN US2004009488-A1.

PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 12; Length 11991;
Best Local Similarity 76.9%; Pred. No. 4.8e-47;
RESULT 490
ID AAS33462 standard; DNA; 25715 BP.
DE DNA encoding human secreted protein, Seq ID No 745.
PN WO200155326-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.8; DB 4; Length 25715;
Best Local Similarity 81.0%; Pred. No. 6.5e-47;
RESULT 491
ID ACN44690 standard; DNA; 47243 BP.
DE Human genomic sequence hCG16501.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201.8; DB 11; Length 47243;
Best Local Similarity 82.3%; Pred. No. 8.2e-47;
RESULT 492
ID ADM97422 standard; DNA; 76341 BP.
DE Prostate and breast cancer associated human gene SRD5A2.
PN WO2004028346-A2.
PD 08-APR-2004.
PA (AMSH-) AMERSHAM BIOSCIENCES SV CORP.
Query Match 22.2%; Score 201.8; DB 12; Length 76341;
Best Local Similarity 83.5%; Pred. No. 9.9e-47;
RESULT 493
ID ADQ9518 standard; DNA; 100762 BP.
DE Human cancer-associated (CA) gene sequence SEQ ID NO:154.
PN WO2004058288-A1.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201.8; DB 13; Length 100762;
Best Local Similarity 78.8%; Pred. No. 1.1e-46;
RESULT 494
Query Match 22.2%; Score 201.8; DB 10; Length 110000;
Best Local Similarity 78.6%; Pred. No. 1.1e-46;
RESULT 495
ID AAD02697 standard; DNA; 160552 BP.
DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
PN WO200106015-A1.
PD 25-JAN-2001.
PA (RESC-) UNIV CALIFORNIA.
Query Match 22.2%; Score 201.8; DB 4; Length 160552;
Best Local Similarity 81.0%; Pred. No. 1.3e-46;
RESULT 496
ID ABD33232 standard; DNA; 161531 BP.
DE Human cancer-associated (CA) gene HD07-038.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201.8; DB 13; Length 161531;
Best Local Similarity 81.0%; Pred. No. 1.3e-46;
RESULT 497
ID ADI33775 standard; DNA; 173805 BP.
DE Osteoarthritis-associated polymorphic nucleotide #307.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.2%; Score 201.8; DB 10; Length 173805;
Best Local Similarity 83.5%; Pred. No. 1.4e-46;
RESULT 498
ID ACN44626 standard; DNA; 175077 BP.
DE Human genomic sequence hCG19724.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201.8; DB 11; Length 175077;
Best Local Similarity 79.9%; Pred. No. 1.4e-46;
RESULT 499
ID ADE43315 standard; DNA; 202100 BP.

DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003
PA (NEUR-) NEUROGENETICS INC.
PA (GENO-) GEN HOSPITAL CORP.
Query Match 22.2%; Score 201.8; DB 10; Length 202100;
Best Local Similarity 81.2%; Pred. No. 1.4e-46;
RESULT 500
ID ADH54357 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GENO-) GEN HOSPITAL CORP.
Query Match 22.2%; Score 201.8; DB 12; Length 202100;
Best Local Similarity 81.2%; Pred. No. 1.4e-46;
RESULT 501
ID ADP75168 standard; DNA; 276820 BP.
DE Human ADAMTS2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 22.2%; Score 201.8; DB 11; Length 276820;
Best Local Similarity 83.7%; Pred. No. 1.6e-46;
RESULT 502
ID AAS32713 standard; DNA; 2666 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 667.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 2666;
Best Local Similarity 77.7%; Pred. No. 3.1e-47;
RESULT 503
ID ADRO6622 standard; cDNA; 3677 BP.
DE Full length human cDNA useful for treating neurological disease Seq 128.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.2%; Score 201.6; DB 13; Length 3677;
Best Local Similarity 83.0%; Pred. No. 3.5e-47;
RESULT 504
ID AAK91537 standard; DNA; 8896 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 5113.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 8896;
Best Local Similarity 77.7%; Pred. No. 4.9e-47;
RESULT 505
ID AAI57794 standard; DNA; 8896 BP.
DE Human colorectal cancer antigen coding sequence SEQ ID NO: 331.
PN WO200155350-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 8896;
Best Local Similarity 77.7%; Pred. No. 4.9e-47;
RESULT 506
ID AAS32712 standard; DNA; 8896 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 666.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 8896;
Best Local Similarity 77.7%; Pred. No. 4.9e-47;
RESULT 507
ID ABS99971 standard; DNA; 8896 BP.
DE Genomic DNA #175 encoding human colorectal cancer related protein.
PN US2002119919-A1.
PD 29-AUG-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.2%; Score 201.6; DB 6; Length 8896;
Best Local Similarity 77.7%; Pred. No. 4.9e-47;

RESULT 508
ID ADB9124 standard; DNA; 8896 BP.
DE Human colorectal cancer related polypeptide DNA #175.
PN US2003054420-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 10; Length 8896;
Best Local Similarity 77.7%; Pred. No. 4.9e-47;
RESULT 509
ID AAL60675 standard; DNA; 12430 BP.
DE Human ataxia telangiectasia and Rad-3-related (ATR) clone8 gene.
PN WO2003044214-A2.
PD 30-MAY-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 22.2%; Score 201.6; DB 9; Length 12430;
Best Local Similarity 85.5%; Pred. No. 5.6e-47;
RESULT 510
ID AAL60676 standard; DNA; 14405 BP.
DE pDC353 knockout construct DNA.
PN WO2003044214-A2.
PD 30-MAY-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 22.2%; Score 201.6; DB 9; Length 14405;
Best Local Similarity 85.5%; Pred. No. 5.9e-47;
RESULT 511
ID AAK84138 standard; DNA; 17758 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38950.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 17758;
Best Local Similarity 83.0%; Pred. No. 6.4e-47;
RESULT 512
ID AAI99172 standard; DNA; 32134 BP.
DE Human excretory related polynucleotide SEQ ID NO 936.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 32134;
Best Local Similarity 77.7%; Pred. No. 8.1e-47;
RESULT 513
ID AAI65522 standard; DNA; 32134 BP.
DE Human kidney related polynucleotide SEQ ID NO 837.
PN WO200155323-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 5; Length 32134;
Best Local Similarity 77.7%; Pred. No. 8.1e-47;
RESULT 514
ID AAI99173 standard; DNA; 32192 BP.
DE Human excretory related polynucleotide SEQ ID NO 937.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 32192;
Best Local Similarity 77.7%; Pred. No. 8.1e-47;
RESULT 515
ID AAI63523 standard; DNA; 32192 BP.
DE Human kidney related polynucleotide SEQ ID NO 838.
PN WO200155323-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 5; Length 32192;
Best Local Similarity 77.7%; Pred. No. 8.1e-47;
RESULT 516
ID AAK69767 standard; DNA; 35100 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24579.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 35100;
Best Local Similarity 77.7%; Pred. No. 8.3e-47;
RESULT 517

ID AAK65700 standard; DNA; 35100 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20512.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 35100;
Best Local Similarity 77.7%; Pred. No. 8.3e-47;
RESULT 518
ID AAK69766 standard; DNA; 35115 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24578.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 35115;
Best Local Similarity 77.7%; Pred. No. 8.3e-47;
RESULT 519
ID AAK65699 standard; DNA; 35115 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20511.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.6; DB 4; Length 35115;
Best Local Similarity 77.7%; Pred. No. 8.3e-47;
RESULT 520
ID ACN44146 standard; DNA; 50602 BP.
DE Human genomic sequence HCG28572.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201.6; DB 11; Length 50602;
Best Local Similarity 81.5%; Pred. No. 9.6e-47;
RESULT 521
ID AAX90201 standard; DNA; 119950 BP.
DE Human yeast gene.
PN WO9935290-A1.
PD 15-JUL-1999.
PA (MILL-) MILLENNium PHARM INC.
Query Match 22.2%; Score 201.6; DB 2; Length 119950;
Best Local Similarity 81.7%; Pred. No. 1.3e-46;
RESULT 522
ID ADP65423 standard; DNA; 154068 BP.
DE Human sequence from clone RP11-363122 on chromosome 1, complete DNA.
PN WO2003072827-A1.
PD 04-SEP-2003.
PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
Query Match 22.2%; Score 201.6; DB 11; Length 154068;
Best Local Similarity 81.2%; Pred. No. 1.5e-46;
RESULT 523
ID ACH21579 standard; cDNA; 406 BP.
DE Human adult liver cDNA #1191.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABART I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 22.2%; Score 201.4; DB 9; Length 406;
Best Local Similarity 82.4%; Pred. No. 1.7e-47;
RESULT 524
ID AAI18654 standard; cDNA; 6020 BP.
DE Human cDNA sequence SEQ ID NO:18887.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 22.2%; Score 201.4; DB 4; Length 6020;
Best Local Similarity 72.9%; Pred. No. 4.8e-47;
RESULT 525
ID AAV34455 standard; DNA; 11722 BP.
DE Human MHC class I chain-related gene A (MICA).
PN WO9819167-A2.
PD 07-MAY-1998.
PA (HOTC-) HUTCHINSON CANCER RES CENT FRED.

Query Match 22.2%; Score 201.4; DB 2; Length 11722;
Best Local Similarity 83.6%; Pred. No. 6.2e-47;
RESULT 526
ID ADE06443 standard; cDNA; 11722 BP.
DE Human MICA cDNA SEQ ID NO:1.
PN WO2003089616-A2.
PD 30-OCT-2003.
PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
Query Match 22.2%; Score 201.4; DB 10; Length 11722;
Best Local Similarity 83.6%; Pred. No. 6.2e-47;
RESULT 527
ID AAK90159 standard; DNA; 15783 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3735.
PN WO200155311-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.4; DB 4; Length 15783;
Best Local Similarity 81.2%; Pred. No. 7e-47;
RESULT 528
ID AAS39803 standard; DNA; 15783 BP.
DE Genomic sequence #222 encoding human colon associated polypeptide.
PN WO200155302-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.4; DB 5; Length 15783;
Best Local Similarity 81.2%; Pred. No. 7e-47;
RESULT 529
ID ADB32763 standard; DNA; 15783 BP.
DE Human novel colon related polypeptide DNA SEQ ID NO 700.
PN US2003050231-A1.
PD 13-MAR-2003.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BAR/) BARASH S C.
Query Match 22.2%; Score 201.4; DB 9; Length 15783;
Best Local Similarity 81.2%; Pred. No. 7e-47;
RESULT 530
ID ABA18491 standard; DNA; 16159 BP.
DE Human nervous system related polynucleotide SEQ ID NO 10822.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.4; DB 5; Length 16159;
Best Local Similarity 85.0%; Pred. No. 7.1e-47;
RESULT 531
ID ACN44470 standard; DNA; 42954 BP.
DE Human genomic sequence hCG40844.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201.4; DB 11; Length 42954;
Best Local Similarity 81.2%; Pred. No. 1e-46;
RESULT 532
ID ADC60735 standard; DNA; 50000 BP.
DE Human slingshot-related DNA 9.
PN JP2003102483-A.
PD 08-APR-2003.
PA (KAG-) KAGAKU GIUTSU SHINKO JIGYODAN.
Query Match 22.2%; Score 201.4; DB 10; Length 50000;
Best Local Similarity 82.4%; Pred. No. 1.1e-46;
RESULT 533
ID ACN44290 standard; DNA; 59856 BP.
DE Human genomic sequence hCG24994.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201.4; DB 11; Length 59856;
Best Local Similarity 81.2%; Pred. No. 1.2e-46;
RESULT 534
ID AAD50739 standard; DNA; 64467 BP.
DE Human Kinase gene.
Query Match 22.2%; Score 201.4; DB 8; Length 64467;
Best Local Similarity 74.6%; Pred. No. 1.2e-46;

RESULT 535
ID ACH00100 standard; DNA; 64467 BP.
DE Human kinase protein genomic DNA.
Query Match 22.2%; Score 201.4; DB 9; Length 64467;
Best Local Similarity 74.6%; Pred. No. 1.2e-46;
RESULT 536
ID ADD15783 standard; DNA; 64467 BP.
DE Human MEK kinase subfamily kinase genomic DNA.
PN US6582946-B1.
PD 24-JUN-2003.
PA (APPL-) APPLERA CORP.
Query Match 22.2%; Score 201.4; DB 10; Length 64467;
Best Local Similarity 74.6%; Pred. No. 1.2e-46;
RESULT 537
ID ABL64403 standard; DNA; 167343 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2740.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 22.2%; Score 201.4; DB 6; Length 167343;
Best Local Similarity 76.1%; Pred. No. 1.7e-46;
RESULT 538
ID ABL67239 standard; DNA; 167343 BP.
DE Thyroid cancer related gene sequence SEQ ID NO:5576.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 22.2%; Score 201.4; DB 6; Length 167343;
Best Local Similarity 76.1%; Pred. No. 1.7e-46;
RESULT 539
ID ABD32715 standard; DNA; 337344 BP.
DE Human cancer-associated genomic DNA HD14-044.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201.4; DB 13; Length 337344;
Best Local Similarity 81.2%; Pred. No. 2.3e-46;
RESULT 540
ID AAH14294 standard; cDNA; 1557 BP.
DE Human cDNA sequence SEQ ID NO:11638.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 22.2%; Score 201.2; DB 4; Length 1557;
Best Local Similarity 85.8%; Pred. No. 3.3e-47;
RESULT 541
ID ADQ19190 standard; DNA; 1557 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2009.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.2%; Score 201.2; DB 12; Length 1557;
Best Local Similarity 85.8%; Pred. No. 3.3e-47;
RESULT 542
ID AAK87586 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42398.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 4; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 543
ID AAK71817 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26629.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 4; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 544
ID AAK73115 standard; DNA; 14426 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27927.
PN WO200157182-A2.

PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 4; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 545
ID AAI62924 standard; DNA; 14426 BP.
DE Human genomic DNA SEQ ID NO 252.
PN WO200155449-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 4; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 546
ID ABZ74676 standard; DNA; 14426 BP.
DE Secreted protein gene 391 genomic fragment HE8FC45, SEQ ID NO:1823.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 8; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 547
ID ABZ68198 standard; DNA; 14426 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1721.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 10; Length 14426;
Best Local Similarity 82.1%; Pred. No. 7.7e-47;
RESULT 548
ID ABA19324 standard; DNA; 27733 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11655.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 5; Length 27733;
Best Local Similarity 79.6%; Pred. No. 9.9e-47;
RESULT 549
ID AAK66517 standard; DNA; 27869 BP.
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:21329.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 4; Length 27869;
Best Local Similarity 76.6%; Pred. No. 9.9e-47;
RESULT 550
ID ABA19635 standard; DNA; 27869 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11966.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201.2; DB 5; Length 27869;
Best Local Similarity 76.6%; Pred. No. 9.9e-47;
RESULT 551
ID ADQ97164 standard; DNA; 145985 BP.
DE Human cancer associated sequence HD1-08-009, SEQ ID 140.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201.2; DB 12; Length 145985;
Best Local Similarity 83.1%; Pred. No. 1.9e-46;
RESULT 552
ID ABD33272 standard; DNA; 227246 BP.
DE Human cancer-associated (CA) gene HD07-047.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201.2; DB 13; Length 227246;
Best Local Similarity 80.7%; Pred. No. 2.2e-46;
RESULT 553
ID AAK65169 standard; DNA; 370 BP.
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:19981.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201; DB 4; Length 370;
Best Local Similarity 81.4%; Pred. No. 2.2e-47;
RESULT 554
ID ABV46137 standard; cDNA; 477 BP.
DE Human prostate expression marker cDNA 46128.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNium PREDICTIVE MEDICINE INC.
Query Match 22.2%; Score 201; DB 5; Length 477;
Best Local Similarity 81.4%; Pred. No. 2.4e-47;
RESULT 555
ID ABQ72599 standard; cDNA; 2616 BP.
DE Human MDR1 encoding cDNA SEQ ID NO 151.
PN WO200240715-A2.
PD 23-MAY-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.2%; Score 201; DB 6; Length 2616;
Best Local Similarity 81.4%; Pred. No. 4.6e-47;
RESULT 556
ID ABD33085 standard; cDNA; 3404 BP.
DE Human cancer-associated (CA) cDNA HR07-004.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201; DB 13; Length 3404;
Best Local Similarity 81.4%; Pred. No. 5.1e-47;
RESULT 557
ID ADJ96554 standard; DNA; 3463 BP.
DE Human calcium/calmodulin-dependent protein kinase Nuak2 DNA SeqID 11.
PN WO2004006838-A2.
PD 22-JAN-2004.
PA (SUG-) SUGEN INC.
Query Match 22.2%; Score 201; DB 12; Length 3463;
Best Local Similarity 81.4%; Pred. No. 5.1e-47;
RESULT 558
ID AAK74096 standard; DNA; 21777 BP.
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:28908.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201; DB 4; Length 21777;
Best Local Similarity 83.9%; Pred. No. 1e-46;
RESULT 559
ID ABA15939 standard; DNA; 24292 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8270.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201; DB 5; Length 24292;
Best Local Similarity 78.7%; Pred. No. 1.1e-46;
RESULT 560
ID AAK66336 standard; DNA; 25971 BP.
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:41148.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.2%; Score 201; DB 4; Length 25971;
Best Local Similarity 73.7%; Pred. No. 1.1e-46;
RESULT 561
ID AAD44328 standard; DNA; 34667 BP.
DE Human transporter gene.
PN WO200248367-A2.
PD 20-JUN-2002.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201; DB 6; Length 34667;
Best Local Similarity 81.4%; Pred. No. 1.2e-46;
RESULT 562
ID ABD33084 standard; DNA; 39699 BP.
DE Human cancer-associated (CA) gene HD07-004.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.2%; Score 201; DB 13; Length 39699;

Best Local Similarity 81.4%; Pred. No. 1.3e-46;
RESULT 563
ID ACN45050 standard; DNA; 41966 BP.
DE Human genomic sequence hCG39344.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.2%; Score 201; DB 11; Length 41966;
Best Local Similarity 83.9%; Pred. No. 1.3e-46;
RESULT 564
ID ABL68262 standard; DNA; 62944 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6599.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALLON PHARM.
Query Match 22.2%; Score 201; DB 6; Length 62944;
Best Local Similarity 78.7%; Pred. No. 1.6e-46;
RESULT 565
ID ABL66947 standard; DNA; 62944 BP.
DE Lung cancer related gene sequence SEQ ID NO:5284.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALLON PHARM.
Query Match 22.2%; Score 201; DB 6; Length 62944;
Best Local Similarity 78.7%; Pred. No. 1.6e-46;
RESULT 566
ID ADL13941 standard; DNA; 125515 BP.
DE Osteoarthritis-associated polymorphic nucleotide #473.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.2%; Score 201; DB 10; Length 125515;
Best Local Similarity 77.2%; Pred. No. 2e-46;
RESULT 567
ID ADC97620 standard; DNA; 144792 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2073.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 22.2%; Score 201; DB 10; Length 144792;
Best Local Similarity 84.5%; Pred. No. 2.1e-46;
RESULT 568
ID ADL13850 standard; DNA; 180550 BP.
DE Osteoarthritis-associated polymorphic nucleotide #382.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.2%; Score 201; DB 10; Length 180550;
Best Local Similarity 81.4%; Pred. No. 2.3e-46;
RESULT 569
ID AB280229 standard; DNA; 249999 BP.
DE Human transmembrane gene region genomic DNA SEQ ID NO:26.
PN WO2003016502-A2.
PD 27-FEB-2003.
PA (MCLA-) MCLAUGHLIN RES INST.
Query Match 22.2%; Score 201; DB 8; Length 249999;
Best Local Similarity 81.4%; Pred. No. 2.6e-46;
RESULT 570
ID ADC87619 standard; DNA; 349981 BP.
DE Human GPCR related polynucleotide SEQ ID NO:2072.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 22.2%; Score 201; DB 10; Length 349981;
Best Local Similarity 84.5%; Pred. No. 3e-46;
RESULT 571
ID ACH29888 standard; cDNA; 390 BP.
DE Human testis cDNA #274.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA-) DRMANAC R T.

PA (LABA-) LABAT I.
PA (STAC-) STACHE-CRAIN B.
PA (DICK-) DICKSON M C.
PA (JONE-) JONES L W.
Query Match 22.1%; Score 200.8; DB 9; Length 390;
Best Local Similarity 84.6%; Pred. No. 2.5e-47;
RESULT 572
ID ADB90993 standard; cDNA; 4421 BP.
DE Human retinal pigment epithelial-derived factor (PDRF) genomic DNA #3.
PN US2003096750-A1.
PD 22-MAY-2003.
PA (TOMB-) TOMBRAN-TINK J.
PA (STEE-) STEELE F R.
PA (CHAD-) CHADER G J.
PA (BECR-) BECERRA S P.
PA (JOHN-) JOHNSON L V.
PA (RODR-) RODRIGUEZ I R.
Query Match 22.1%; Score 200.8; DB 10; Length 4421;
Best Local Similarity 80.7%; Pred. No. 6.4e-47;
RESULT 573
ID ABS57269 standard; DNA; 4421 BP.
DE Partial sequence #3 of genomic DNA encoding human PEDF.
PN US6451763-B1.
PD 17-SEP-2002.
PA (USSH-) US DEPT HEALTH & HUMAN SERVICES.
Query Match 22.1%; Score 200.8; DB 10; Length 4421;
Best Local Similarity 80.7%; Pred. No. 6.4e-47;
RESULT 574
ID AAK9727 standard; DNA; 22645 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3303.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.8; DB 4; Length 22645;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
RESULT 575
ID AAL05495 standard; DNA; 22645 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 0183.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.8; DB 4; Length 22645;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
RESULT 576
ID AAL04985 standard; DNA; 22645 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7673.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.8; DB 4; Length 22645;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
RESULT 577
ID ABL97878 standard; DNA; 22645 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 2530.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.8; DB 4; Length 22645;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
RESULT 578
ID ABL98348 standard; DNA; 22645 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3000.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.8; DB 4; Length 22645;
Best Local Similarity 79.9%; Pred. No. 1.2e-46;
RESULT 579
ID AAK66931 standard; DNA; 30620 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21743.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.1%; Score 200.8; DB 4; Length 30620;
Best Local Similarity 80.9%; Pred. No. 1.3e-46;
RESULT 580
ID ADA02600 standard; DNA; 96593 BP.
DE Human RUNX1 carcinoma associated gene, SEQ ID NO:1118.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.8; DB 9; Length 96593;
Best Local Similarity 85.8%; Pred. No. 2.1e-46;
RESULT 581
ID ADB72338 standard; DNA; 96593 BP.
DE Human RUNX1 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.8; DB 10; Length 96593;
Best Local Similarity 85.8%; Pred. No. 2.1e-46;
RESULT 582
ID ADB95848 standard; DNA; 96593 BP.
DE Human RUNX1 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.8; DB 10; Length 96593;
Best Local Similarity 85.8%; Pred. No. 2.1e-46;
RESULT 583
ID AAD1230 standard; DNA; 107820 BP.
DE Human ATP-binding cassette transporter ABC6 (MR6) complementary gene.
Query Match 22.1%; Score 200.8; DB 4; Length 107820;
Best Local Similarity 84.9%; Pred. No. 2.2e-46;
RESULT 584
ID ACF6273 standard; DNA; 172984 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:661.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200.8; DB 8; Length 172984;
Best Local Similarity 84.9%; Pred. No. 2.6e-46;
RESULT 585
ID ADB20848 standard; DNA; 172984 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:661.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200.8; DB 8; Length 172984;
Best Local Similarity 84.9%; Pred. No. 2.6e-46;
RESULT 586
ID ADB87937 standard; DNA; 172984 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:661.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200.8; DB 10; Length 172984;
Best Local Similarity 84.9%; Pred. No. 2.6e-46;
RESULT 587
ID ADB96920 standard; DNA; 172984 BP.
DE Human MDRI related DNA sequence SEQ ID NO:661.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200.8; DB 10; Length 172984;
Best Local Similarity 84.9%; Pred. No. 2.6e-46;
RESULT 588
ID ADB92111 standard; DNA; 172984 BP.
DE Human MDRI related DNA sequence SEQ ID NO:661.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200.8; DB 10; Length 172984;
Best Local Similarity 84.9%; Pred. No. 2.6e-46;
RESULT 589
ID ADO97167 standard; DNA; 176771 BP.

DE Human cancer associated sequence HD2-08-009, SEQ ID 143.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200.8; DB 12; Length 176771;
Best Local Similarity 75.9%; Pred. No. 2.6e-46;
RESULT 590
ID ACN44418 standard; DNA; 213040 BP.
DE Human genomic sequence hCG41574.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.8; DB 11; Length 213040;
Best Local Similarity 83.3%; Pred. No. 2.8e-46;
RESULT 591
ID AAH51601 standard; DNA; 319608 BP.
DE Human chromosome 13q31-q33 genomic nucleotide sequence.
PN WO200058510-A2.
PD 05-OCT-2000.
PA (GEST) GENSET.
Query Match 22.1%; Score 200.8; DB 3; Length 319608;
Best Local Similarity 84.7%; Pred. No. 3.3e-46;
RESULT 592
ID AAS09301 standard; DNA; 319608 BP.
DE Human schizophrenia associated gene q35030 and biallelic markers A1-A71.
Query Match 22.1%; Score 200.8; DB 5; Length 319608;
Best Local Similarity 84.7%; Pred. No. 3.3e-46;
RESULT 593
ID AAK84440 standard; DNA; 2821 BP.
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:39252.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.6; DB 4; Length 2821;
Best Local Similarity 84.2%; Pred. No. 6.1e-47;
RESULT 594
ID AAS32797 standard; DNA; 5668 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 751.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.6; DB 4; Length 5668;
Best Local Similarity 83.0%; Pred. No. 8e-47;
RESULT 595
ID AAK42719 standard; DNA; 8894 BP.
DE Genomic sequence #618 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.6; DB 4; Length 8894;
Best Local Similarity 81.2%; Pred. No. 9.5e-47;
RESULT 596
ID ADB60875 standard; DNA; 8894 BP.
DE Connective tissue related genomic DNA #618.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.6; DB 9; Length 8894;
Best Local Similarity 81.2%; Pred. No. 9.5e-47;
RESULT 597
ID AOS36489 standard; DNA; 14902 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1703.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.1%; Score 200.6; DB 13; Length 14902;
Best Local Similarity 81.4%; Pred. No. 1.2e-46;
RESULT 598
ID ACN45210 standard; DNA; 48680 BP.
DE Human genomic sequence hCG37835.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 22.1%; Score 200.6; DB 11; Length 48680;
Best Local Similarity 84.2%; Pred. No. 1.8e-46;
RESULT 599
ID ACA60949 standard; DNA; 55827 BP.
DE DNA encoding human carboxypeptidase.
PN US2003017574-A1.
Query Match 22.1%; Score 200.6; DB 8; Length 55827;
Best Local Similarity 81.4%; Pred. No. 1.9e-46;
RESULT 600
ID ABX13671 standard; DNA; 55827 BP.
DE Human protease gene.
Query Match 22.1%; Score 200.6; DB 10; Length 55827;
Best Local Similarity 81.4%; Pred. No. 1.9e-46;
RESULT 601
ID ADL27146 standard; DNA; 96593 BP.
DE Human genomic sequence for PPP3CC.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGER/) ENGERHARD E K.
Query Match 22.1%; Score 200.6; DB 11; Length 96593;
Best Local Similarity 81.6%; Pred. No. 2.4e-46;
RESULT 602
ID ADA03068 standard; DNA; 96595 BP.
DE Human PPP3CC carcinoma associated gene, SEQ ID NO:1586.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.6; DB 9; Length 96595;
Best Local Similarity 81.6%; Pred. No. 2.4e-46;
RESULT 603
ID ADB72806 standard; DNA; 96595 BP.
DE Human PPP3CC gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.6; DB 10; Length 96595;
Best Local Similarity 81.6%; Pred. No. 2.4e-46;
RESULT 604
ID ADA66352 standard; DNA; 96596 BP.
DE Human PPP3CC gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.6; DB 9; Length 96596;
Best Local Similarity 81.6%; Pred. No. 2.4e-46;
RESULT 605
ID ADJ79961 standard; DNA; 106344 BP.
DE Full length human glioma-associated oncogene-3 DNA, SEQ ID NO 10.
PN WO2003008549-A2.
PD 30-JAN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 22.1%; Score 200.6; DB 10; Length 106344;
Best Local Similarity 85.5%; Pred. No. 2.5e-46;
RESULT 606
ID ACN44758 standard; DNA; 172569 BP.
DE Human genomic sequence hCG20145.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.6; DB 11; Length 172569;
Best Local Similarity 79.4%; Pred. No. 3e-46;
RESULT 607
ID ABQ88207 standard; cDNA; 172570 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 114.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC) PROCTER & GAMBLE CO.
Query Match 22.1%; Score 200.6; DB 6; Length 172570;
Best Local Similarity 80.3%; Pred. No. 3e-46;
RESULT 608
ID ADL13512 standard; DNA; 178870 BP.

DE Osteoarthritis-associated polymorphic nucleotide #44.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.1%; Score 200.6; DB 10; Length 178870;
Best Local Similarity 83.0%; Pred. No. 3e-46;
RESULT 609
ID ACN44046 standard; DNA; 260027 BP.
DE Human genomic sequence hCG1735292.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.6; DB 11; Length 260027;
Best Local Similarity 83.0%; Pred. No. 3.5e-46;
RESULT 610
ID ABL41258 standard; cDNA; 1689 BP.
DE Human cytochrome bcl compound core protein IT10.34 encoding cDNA.
PN CN1325876-A.
PD 12-DEC-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match 22.1%; Score 200.4; DB 6; Length 1689;
Best Local Similarity 77.9%; Pred. No. 5.7e-47;
RESULT 611
ID AAH15160 standard; cDNA; 1739 BP.
DE Human cDNA sequence SEQ ID NO:13234.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 22.1%; Score 200.4; DB 4; Length 1739;
Best Local Similarity 83.7%; Pred. No. 5.8e-47;
RESULT 612
ID ABK69090 standard; cDNA; 2952 BP.
DE DNA encoding human secreted protein, SEQ ID NO 14.
PN WO200224721-A1.
PD 28-MAR-2002.
PA (HUMA-) HUMA GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 6; Length 2952;
Best Local Similarity 78.2%; Pred. No. 7.1e-47;
RESULT 613
ID ADQ64569 standard; cDNA; 3341 BP.
DE Novel human cDNA sequence #1730.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.1%; Score 200.4; DB 12; Length 3341;
Best Local Similarity 85.2%; Pred. No. 7.5e-47;
RESULT 614
ID ADJ78567 standard; DNA; 13278 BP.
DE Human cytochrome P450 isoenzyme 2D6 pseudogene Seg1D5.
PN WO2004009760-A2.
PD 29-JAN-2004.
PA (BIOV-) BIOVENTURES INC.
Query Match 22.1%; Score 200.4; DB 12; Length 13278;
Best Local Similarity 80.2%; Pred. No. 1.3e-46;
RESULT 615
ID ADM28895 standard; DNA; 13278 BP.
DE Human pseudogene #2 located near CYP2D6 gene.
PN US2004072235-A1.
PD 15-APR-2004.
PA (DAMS/) DAWSON E P.
Query Match 22.1%; Score 200.4; DB 12; Length 13278;
Best Local Similarity 80.2%; Pred. No. 1.3e-46;
RESULT 616
ID ADJ78568 standard; DNA; 13677 BP.
DE Human cytochrome P450 isoenzyme 2D6 pseudogene Seg1D6.
PN WO2004009760-A2.
PD 29-JAN-2004.
PA (BIOV-) BIOVENTURES INC.
Query Match 22.1%; Score 200.4; DB 12; Length 13677;
Best Local Similarity 80.2%; Pred. No. 1.3e-46;
RESULT 617
ID ADM28896 standard; DNA; 13677 BP.
DE Human pseudogene #3 located near CYP2D6 gene.

PN US2004072235-A1.
PD 15-APR-2004.
PA (DAMSON E P.
Query Match 22.1%; Score 200.4; DB 12; Length 13677;
Best Local Similarity 80.2%; Pred. No. 1.3e-46;
RESULT 618
ID AAI62664 standard; DNA; 21936 BP.
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 314.
PN WO200155324-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 4; Length 21936;
Best Local Similarity 82.5%; Pred. No. 1.5e-46;
RESULT 619
ID AAL06758 standard; DNA; 21936 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9446.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 4; Length 21936;
Best Local Similarity 82.5%; Pred. No. 1.5e-46;
RESULT 620
ID AAL06119 standard; DNA; 21936 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8807.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 4; Length 21936;
Best Local Similarity 82.5%; Pred. No. 1.5e-46;
RESULT 621
ID ABL9684 standard; DNA; 21936 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3336.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 4; Length 21936;
Best Local Similarity 82.5%; Pred. No. 1.5e-46;
RESULT 622
ID ABA15865 standard; DNA; 21936 BP.
DE Human nervous system related polynucleotide SEQ ID NO: 8196.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.4; DB 5; Length 21936;
Best Local Similarity 82.5%; Pred. No. 1.5e-46;
RESULT 623
ID AAI72317 standard; cDNA; 26657 BP.
DE Human transporter protein gene.
PN WO200202635-A2.
PD 10-JAN-2002.
PA (APPL-) APPLERA CORP.
Query Match 22.1%; Score 200.4; DB 6; Length 26657;
Best Local Similarity 80.9%; Pred. No. 1.7e-46;
RESULT 624
ID ABD32649 standard; DNA; 102790 BP.
DE Human cancer-associated genomic DNA HD13-036.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200.4; DB 13; Length 102790;
Best Local Similarity 82.3%; Pred. No. 2.8e-46;
RESULT 625
ID ABD32811 standard; DNA; 161051 BP.
DE Human cancer-associated genomic DNA HD16-063.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200.4; DB 13; Length 161051;
Best Local Similarity 85.2%; Pred. No. 3.3e-46;
RESULT 626
ID ACN44626 standard; DNA; 175077 BP.
DE Human genomic sequence hCG19724.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200.4; DB 11; Length 175077;
Best Local Similarity 82.3%; Pred. No. 3.4e-46;
RESULT 627
ID AAD58279 standard; DNA; 226475 BP.
DE Human tumour suppressor gene, Lmt reverse complement DNA.
PN WO200306689-A1.
PD 14-AUG-2003.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELITZ.
Query Match 22.1%; Score 200.4; DB 9; Length 226475;
Best Local Similarity 81.1%; Pred. No. 3.8e-46;
RESULT 628
ID ABR83497 standard; cDNA; 227968 BP.
DE Human cDNA differentially expressed in granulocytic cells #68.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 22.1%; Score 200.4; DB 6; Length 227968;
Best Local Similarity 82.5%; Pred. No. 3.8e-46;
RESULT 629
ID ADQ18538 standard; DNA; 227968 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1357.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.1%; Score 200.4; DB 12; Length 227968;
Best Local Similarity 82.5%; Pred. No. 3.8e-46;
RESULT 630
ID ADS64405 standard; DNA; 601 BP.
DE Human transporter protein encoding gene fragment #11.
PN US2004191829-A1.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.1%; Score 200.2; DB 13; Length 601;
Best Local Similarity 81.1%; Pred. No. 4.4e-47;
RESULT 631
ID AAK71508 standard; DNA; 781 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 26320.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 4; Length 781;
Best Local Similarity 80.7%; Pred. No. 4.9e-47;
RESULT 632
ID AAK71507 standard; DNA; 796 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 26319.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 4; Length 796;
Best Local Similarity 80.7%; Pred. No. 4.9e-47;
RESULT 633
ID AAK86179 standard; DNA; 3341 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 40991.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 4; Length 3341;
Best Local Similarity 76.5%; Pred. No. 8.5e-47;
RESULT 634
ID AAK86178 standard; DNA; 3341 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 40990.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 4; Length 3341;
Best Local Similarity 78.5%; Pred. No. 8.5e-47;
RESULT 635
ID AAK85916 standard; DNA; 4553 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 40728.
PN WO200157182-A2.
PD 09-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 4; Length 4553;
Best Local Similarity 83.2%; Pred. No. 9.6e-47;
RESULT 636
ID AAF97858 standard; DNA; 10709 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:72.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM-) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 22.1%; Score 200.2; DB 5; Length 10709;
Best Local Similarity 84.6%; Pred. No. 1.3e-46;
RESULT 637
ID AAF97857 standard; DNA; 13646 BP.
DE Human neuroblastoma cell line NB-1 1p36 nucleotide sequence SEQ ID NO:71.
PN WO200116311-A1.
PD 08-MAR-2001.
PA (HISM-) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
Query Match 22.1%; Score 200.2; DB 5; Length 13646;
Best Local Similarity 84.6%; Pred. No. 1.5e-46;
RESULT 638
ID ABA15431 standard; DNA; 25012 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7762.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 5; Length 25012;
Best Local Similarity 81.1%; Pred. No. 1.9e-46;
RESULT 639
ID AB273798 standard; DNA; 25012 BP.
DE Secreted protein gene 42 genomic fragment HBMTM11, SEQ ID NO:945.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 8; Length 25012;
Best Local Similarity 81.1%; Pred. No. 1.9e-46;
RESULT 640
ID ADA88470 standard; DNA; 25012 BP.
DE Human secreted protein-related DNA sequence #63.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.1%; Score 200.2; DB 8; Length 25012;
Best Local Similarity 81.1%; Pred. No. 1.9e-46;
RESULT 641
ID ACN44118 standard; DNA; 31652 BP.
DE Human genomic sequence hCG23908.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200.2; DB 11; Length 31652;
Best Local Similarity 70.8%; Pred. No. 2e-46;
RESULT 642
ID ADC87688 standard; DNA; 37138 BP.
DE Human mammalian target of rapamycin genomic fragment #33.
PN WO2003068350-A1.
PD 12-JUN-2003.
PA (NEMI-) NEM IND RES ORG.
Query Match 22.1%; Score 200.2; DB 10; Length 37138;
Best Local Similarity 79.1%; Pred. No. 2.2e-46;
RESULT 643
ID ADS36454 standard; DNA; 58337 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1668.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.1%; Score 200.2; DB 13; Length 58337;
Best Local Similarity 81.1%; Pred. No. 2.6e-46;
RESULT 644
ID ABD33260 standard; DNA; 59748 BP.
DE Human cancer-associated (CA) gene HD07-044.
PN WO2004058146-A2.

PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200.2; DB 13; Length 59748;
Best Local Similarity 71.7%; Pred. No. 2.6e-46;
RESULT 645
ID ADS36462 standard; DNA; 64423 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1676.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.1%; Score 200.2; DB 13; Length 64423;
Best Local Similarity 81.1%; Pred. No. 2.7e-46;
RESULT 646
ID AAA10225 standard; DNA; 106746 BP.
DE Human PCTA-1 genomic DNA, SEQ ID NO:1.
PN WO9964590-A1.
PD 16-DEC-1999.
PA (GEST-) GENSET.
Query Match 22.1%; Score 200.2; DB 3; Length 106746;
Best Local Similarity 83.2%; Pred. No. 3.2e-46;
RESULT 647
Query Match 22.1%; Score 200.2; DB 12; Length 110000;
Best Local Similarity 83.2%; Pred. No. 3.3e-46;
RESULT 648
ID ADA42607 standard; DNA; 113604 BP.
DE Human LOTS genomic DNA #2.
PN US2003077633-A1.
PD 24-APR-2003.
PA (PERL-) PERLEGEN SCI INC.
Query Match 22.1%; Score 200.2; DB 9; Length 113604;
Best Local Similarity 78.8%; Pred. No. 3.3e-46;
RESULT 649
ID ADA42606 standard; DNA; 113604 BP.
DE Human LOTS genomic DNA #1.
PN US2003077633-A1.
PD 24-APR-2003.
PA (PERL-) PERLEGEN SCI INC.
Query Match 22.1%; Score 200.2; DB 9; Length 113604;
Best Local Similarity 78.8%; Pred. No. 3.3e-46;
RESULT 650
ID ADS19853 standard; DNA; 113604 BP.
DE Human chromosome 21 nucleotide sequence SEQ ID NO:1.
PN WO2004018701-A2.
PD 04-MAR-2004.
PA (PERL-) PERLEGEN SCI INC.
PA (COXD/) COX D R.
PA (ARNO/) ARNOLD D A.
Query Match 22.1%; Score 200.2; DB 13; Length 113604;
Best Local Similarity 78.8%; Pred. No. 3.3e-46;
RESULT 651
ID ADS19854 standard; DNA; 113604 BP.
DE Human chromosome 21 nucleotide sequence SEQ ID NO:2.
PN WO2004018701-A2.
PD 04-MAR-2004.
PA (PERL-) PERLEGEN SCI INC.
PA (COXD/) COX D R.
PA (ARNO/) ARNOLD D A.
Query Match 22.1%; Score 200.2; DB 13; Length 113604;
Best Local Similarity 78.8%; Pred. No. 3.3e-46;
RESULT 652
ID AAC6548 standard; DNA; 121162 BP.
DE Human kinesin-like protein HKLP coding sequence contig SEQ ID NO: 1.
PN WO200063375-A1.
PD 26-OCT-2000.
PA (GEST-) GENSET.
Query Match 22.1%; Score 200.2; DB 3; Length 121162;
Best Local Similarity 84.6%; Pred. No. 3.4e-46;
RESULT 653
ID ACN44966 standard; DNA; 125534 BP.
DE Human genomic sequence hCG32986.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.

Query Match 22.1%; Score 200.2; DB 11; Length 125534;
 Best Local Similarity 82.2%; Pred. No. 3.4e-46;
 RESULT 654
 ID ACN44142 standard; DNA; 143973 BP.
 DE Human genomic sequence hCG1546502.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.1%; Score 200.2; DB 11; Length 143973;
 Best Local Similarity 78.5%; Pred. No. 3.6e-46;
 RESULT 655
 ID ABQ77400 standard; DNA; 174566 BP.
 DE Human ITGB3 DNA.
 PN WO2003016494-A2.
 PD 27-FEB-2003.
 PA (VITI-) VITIVITY INC.
 Query Match 22.1%; Score 200.2; DB 8; Length 174566;
 Best Local Similarity 83.0%; Pred. No. 3.9e-46;
 RESULT 656
 ID ADL08118 standard; DNA; 174566 BP.
 DE Human gene associated with low HDL-C ITGB3.
 PN US2004043389-A1.
 PD 04-MAR-2004.
 PA (VITI-) VITIVITY INC.
 Query Match 22.1%; Score 200.2; DB 12; Length 174566;
 Best Local Similarity 83.0%; Pred. No. 3.9e-46;
 RESULT 657
 ID ACN44650 standard; DNA; 256157 BP.
 DE Human genomic sequence hCG38672.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.1%; Score 200.2; DB 11; Length 256157;
 Best Local Similarity 83.0%; Pred. No. 4.5e-46;
 RESULT 658
 ID ABD35570 standard; DNA; 256157 BP.
 DE Human cancer-associated (CA) gene HD07-114.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.1%; Score 200.2; DB 13; Length 256157;
 Best Local Similarity 83.0%; Pred. No. 4.5e-46;
 RESULT 659
 ID ADO26258 standard; DNA; 1061 BP.
 DE C35 promoter and polynucleotide targeting method related human DNA #1.
 PN WO2004037993-A2.
 PD 06-MAY-2004.
 PA (UYRP) UNIV ROCHESTER.
 PA (ZAUD/) ZAUDERER M.
 PA (PARI/) PARIS M.
 Query Match 22.1%; Score 200; DB 12; Length 1061;
 Best Local Similarity 81.3%; Pred. No. 6.3e-47;
 RESULT 660
 ID ADO26269 standard; DNA; 1107 BP.
 DE Human breast cancer associated C35 promoter.
 PN WO2004037993-A2.
 PD 06-MAY-2004.
 PA (UYRP) UNIV ROCHESTER.
 PA (ZAUD/) ZAUDERER M.
 PA (PARI/) PARIS M.
 Query Match 22.1%; Score 200; DB 12; Length 1107;
 Best Local Similarity 81.3%; Pred. No. 6.4e-47;
 RESULT 661
 ID ABQ83751 standard; cDNA; 1812 BP.
 DE Human nucleotide reductase 16.83 encoding cDNA SEQ ID NO:1.
 PN CN1347989-A.
 PD 08-MAY-2002.
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 Query Match 22.1%; Score 200; DB 6; Length 1812;
 Best Local Similarity 81.3%; Pred. No. 7.7e-47;
 RESULT 662
 ID ADO26370 standard; DNA; 7401 BP.
 DE C35 promoter and polynucleotide targeting method related human DNA #12.

PN WO2004037993-A2.
 PD 06-MAY-2004.
 PA (UYRP) UNIV ROCHESTER.
 PA (ZAUD/) ZAUDERER M.
 PA (PARI/) PARIS M.
 Query Match 22.1%; Score 200; DB 12; Length 7401;
 Best Local Similarity 81.3%; Pred. No. 1.3e-46;
 RESULT 663
 ID AAK1538 standard; DNA; 8895 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 5114.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200; DB 4; Length 8895;
 Best Local Similarity 77.5%; Pred. No. 1.4e-46;
 RESULT 664
 ID AA157795 standard; DNA; 8895 BP.
 DE Human colorectal cancer antigen coding sequence SEQ ID NO: 332.
 PN WO200155350-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200; DB 4; Length 8895;
 Best Local Similarity 77.5%; Pred. No. 1.4e-46;
 RESULT 665
 ID AAS37714 standard; DNA; 8895 BP.
 DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 668.
 PN WO200155319-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200; DB 4; Length 8895;
 Best Local Similarity 77.5%; Pred. No. 1.4e-46;
 RESULT 666
 ID ABS99972 standard; DNA; 8895 BP.
 DE Genomic DNA #176 encoding human colorectal cancer related protein.
 PN US2002119919-A1.
 PD 29-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 22.1%; Score 200; DB 6; Length 8895;
 Best Local Similarity 77.5%; Pred. No. 1.4e-46;
 RESULT 667
 ID ADB93125 standard; DNA; 8895 BP.
 DE Human colorectal cancer related polypeptide DNA #176.
 PN US2003014340-A2.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.1%; Score 200; DB 10; Length 8895;
 Best Local Similarity 77.5%; Pred. No. 1.4e-46;
 RESULT 668
 ID ACC00503 standard; DNA; 23434 BP.
 DE Human histone deacetylase HDAC10 genomic DNA sequence, SEQ ID NO:4.
 PN WO2003014340-A2.
 PD 20-FEB-2003.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 Query Match 22.1%; Score 200; DB 8; Length 23434;
 Best Local Similarity 78.1%; Pred. No. 2.1e-46;
 RESULT 669
 ID ADF90165 standard; DNA; 46649 BP.
 DE Genomic DNA encoding human transporter protein.
 PN WO2003014340-A2.
 PD 20-FEB-2003.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 Query Match 22.1%; Score 200; DB 10; Length 46649;
 Best Local Similarity 79.1%; Pred. No. 2.7e-46;
 RESULT 670
 ID ADR03800 standard; DNA; 46649 BP.
 DE Human gene encoding a novel transporter.
 PN WO2003014340-A2.
 PD 20-FEB-2003.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 Query Match 22.1%; Score 200; DB 13; Length 46649;
 Best Local Similarity 79.1%; Pred. No. 2.7e-46;
 RESULT 671
 ID ACN45002 standard; DNA; 60430 BP.
 DE Human genomic sequence hCG33210.
 PN WO2003073826-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200; DB 11; Length 60430;
Best Local Similarity 80.9%; Pred. No. 3e-46;
RESULT 672
ID ABK94411 standard; DNA; 109906 BP.
DE cDNA encoding endochelin converting enzyme 1 (ECE-1) #1.
PN WO200224747-A2.
PD 28-MAR-2002.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.1%; Score 200; DB 6; Length 109906;
Best Local Similarity 85.4%; Pred. No. 3.7e-46;
RESULT 673
ID ADL08112 standard; DNA; 109906 BP.
DE Human gene associated with low HDL-C ECE1.
PN US200404389-A1.
PD 04-MAR-2004.
PA (VITI-) VITIVITY INC.
Query Match 22.1%; Score 200; DB 12; Length 109906;
Best Local Similarity 85.4%; Pred. No. 3.7e-46;
RESULT 674
ID ABD32806 standard; DNA; 653458 BP.
DE Human cancer-associated genomic DNA HD16-059.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200; DB 13; Length 110000;
Best Local Similarity 75.0%; Pred. No. 3.7e-46;
RESULT 675
ID ACN44334 standard; DNA; 161334 BP.
DE Human genomic sequence hCG32959.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.1%; Score 200; DB 11; Length 161334;
Best Local Similarity 85.4%; Pred. No. 4.3e-46;
RESULT 676
ID ABD32688 standard; DNA; 208700 BP.
DE Human cancer-associated genomic DNA HD14-005.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.1%; Score 200; DB 13; Length 208700;
Best Local Similarity 80.4%; Pred. No. 4.8e-46;
RESULT 677
ID ADL3684 standard; DNA; 247509 BP.
DE Osteoarthritis-associated polymorphic nucleotide #216.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.1%; Score 200; DB 10; Length 247509;
Best Local Similarity 81.3%; Pred. No. 5.1e-46;
RESULT 678
ID ADP75180 standard; DNA; 304905 BP.
DE Human Endophilin 2 gene.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 22.1%; Score 200; DB 11; Length 304905;
Best Local Similarity 74.3%; Pred. No. 5.5e-46;
RESULT 679
ID AAA02015 standard; cDNA; 711 BP.
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:2006.
PN WO958675-A2.
PD 18-NOV-1999.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.8; DB 3; Length 711;
Best Local Similarity 82.8%; Pred. No. 6.1e-47;
RESULT 680
ID AAL37239 standard; DNA; 2306 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3604.
PN WO200155367-A1.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 4; Length 2306;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 681
ID ABK60227 standard; cDNA; 2306 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2571.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.0%; Score 199.8; DB 8; Length 2306;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 682
ID ADJ30977 standard; DNA; 2306 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3604.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 12; Length 2306;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 683
ID AAL37240 standard; DNA; 2311 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3605.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 4; Length 2311;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 684
ID ABK60228 standard; cDNA; 2311 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2572.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.0%; Score 199.8; DB 8; Length 2311;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 685
ID ADJ30978 standard; DNA; 2311 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3605.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 12; Length 2311;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 686
ID AAL37241 standard; DNA; 2312 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 3606.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 4; Length 2312;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 687
ID ABK60229 standard; cDNA; 2312 BP.
DE cDNA encoding novel human musculoskeletal system antigen #2573.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.0%; Score 199.8; DB 8; Length 2312;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;
RESULT 688
ID ADJ30979 standard; DNA; 2312 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3606.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.8; DB 12; Length 2312;
Best Local Similarity 81.1%; Pred. No. 9.6e-47;

RESULT 689
 ID ADO24272 standard; DNA; 3364 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7092.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 22.0%; Score 199.8; DB 12; Length 3364;
 Best Local Similarity 80.9%; Pred. No. 1.1e-46;
 RESULT 690
 ID AAI61061 standard; cDNA; 3775 BP.
 DE Human polynucleotide SEQ ID NO 5050.
 PN WO200153312-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSSEQ INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 3775;
 Best Local Similarity 83.3%; Pred. No. 1.2e-46;
 RESULT 691
 ID AAK74057 standard; DNA; 5024 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28869.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 5024;
 Best Local Similarity 83.4%; Pred. No. 1.3e-46;
 RESULT 692
 ID AAK74056 standard; DNA; 5024 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28868.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 5024;
 Best Local Similarity 83.4%; Pred. No. 1.3e-46;
 RESULT 693
 ID ADC86878 standard; DNA; 10102 BP.
 DE Human GPCR gene SEQ ID NO:1331.
 PN EPI270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATOR.
 Query Match 22.0%; Score 199.8; DB 10; Length 10102;
 Best Local Similarity 86.2%; Pred. No. 1.7e-46;
 RESULT 694
 ID AAS27797 standard; DNA; 18449 BP.
 DE DNA encoding novel signal transduction pathway protein, Seq ID 1457.
 PN WO200154733-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 18449;
 Best Local Similarity 80.9%; Pred. No. 2.1e-46;
 RESULT 695
 ID ABA20913 standard; DNA; 18449 BP.
 DE Human nervous system related polynucleotide SEQ ID NO 13244.
 PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 5; Length 18449;
 Best Local Similarity 80.9%; Pred. No. 2.1e-46;
 RESULT 696
 ID ADB94600 standard; DNA; 18449 BP.
 DE Novel human protein DNA #209.
 PN US2002168711-A1.
 PD 14-NOV-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 22.0%; Score 199.8; DB 10; Length 18449;
 Best Local Similarity 80.9%; Pred. No. 2.1e-46;
 RESULT 697
 ID ACN44810 standard; DNA; 25668 BP.
 DE Human genomic sequence hc28302.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.

Query Match 22.0%; Score 199.8; DB 11; Length 25668;
 Best Local Similarity 80.9%; Pred. No. 2.4e-46;
 RESULT 698
 ID ABA07160 standard; DNA; 31931 BP.
 DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 479.
 PN WO200155206-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 4; Length 31931;
 Best Local Similarity 83.3%; Pred. No. 2.6e-46;
 RESULT 699
 ID ADC20666 standard; DNA; 51961 BP.
 DE Human secreted protein-related DNA sequence #84.
 PN WO200292787-A2.
 PD 21-NOV-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 10; Length 51961;
 Best Local Similarity 83.3%; Pred. No. 3.2e-46;
 RESULT 700
 ID ABT16905 standard; DNA; 51961 BP.
 DE Human secreted protein-related DNA sequence - SEQ ID NO 259.
 PN WO200277188-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 10; Length 51961;
 Best Local Similarity 83.3%; Pred. No. 3.2e-46;
 RESULT 701
 ID ABZ67488 standard; DNA; 51961 BP.
 DE Human secreted protein encoding genomic DNA SEQ ID NO 1011.
 PN WO200277188-A2.
 PD 03-OCT-2002.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 22.0%; Score 199.8; DB 10; Length 51961;
 Best Local Similarity 83.3%; Pred. No. 3.2e-46;
 RESULT 702
 ID ADE95902 standard; DNA; 94720 BP.
 DE Human STRAT5B gene genomic DNA sequence.
 PN WO2003039484-A2.
 PD 15-MAY-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.8; DB 10; Length 94720;
 Best Local Similarity 81.1%; Pred. No. 4e-46;
 RESULT 703
 ID ADA02654 standard; DNA; 94720 BP.
 DE Human STRAT5B carcinoma associated gene, SEQ ID NO:1172.
 PN WO2003057146-A2.
 PD 17-JUL-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.8; DB 9; Length 94720;
 Best Local Similarity 81.1%; Pred. No. 4e-46;
 RESULT 704
 ID ADB72392 standard; DNA; 94720 BP.
 DE Human STRAT5B gene.
 PN WO2003008583-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 22.0%; Score 199.8; DB 10; Length 94720;
 Best Local Similarity 81.1%; Pred. No. 4e-46;
 RESULT 705
 ID ADQ97846 standard; DNA; 94911 BP.
 DE Human cancer associated sequence HDL1-010, SEQ ID 823.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 22.0%; Score 199.8; DB 12; Length 94911;
 Best Local Similarity 79.7%; Pred. No. 4e-46;
 RESULT 706
 ID ADN06353 standard; DNA; 398800 BP.
 DE Human FLAP genomic DNA SEQ ID NO:1.
 PN WO2004035741-A2.
 PD 29-APR-2004.
 PA (DECO-) DECODE GENETICS BHF.
 Query Match 22.0%; Score 199.8; DB 12; Length 110000;

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Best Local Similarity 80.9%; Pred. No. 4.3e-46;
RESULT 707
ID ADS94372 standard; DNA; 398800 BP.
DE Human 5-lipoxygenase activating protein (FLAP) gene.
PN WO2004035746-A2.
PD 29-APR-2004.
PA (DECO-) DECODE GENETICS EHF.
Query Match 22.0%; Score 199.8; DB 13; Length 110000;
Best Local Similarity 80.9%; Pred. No. 4.3e-46;
RESULT 708
ID ACN44026 standard; DNA; 122923 BP.
DE Human genomic sequence hCG24510.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.8; DB 11; Length 122923;
Best Local Similarity 80.9%; Pred. No. 4.5e-46;
RESULT 709
ID ADQ21602 standard; DNA; 131673 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4422.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.0%; Score 199.8; DB 12; Length 131673;
Best Local Similarity 84.6%; Pred. No. 4.6e-46;
RESULT 710
ID ADQ9389 standard; DNA; 155937 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2208.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 22.0%; Score 199.8; DB 12; Length 155937;
Best Local Similarity 83.0%; Pred. No. 4.9e-46;
RESULT 711
ID AAD02697 standard; DNA; 160552 BP.
DE Human glycosyl sulfotransferase-4 (GST-4) genomic DNA.
PN WO200106015-A1.
PD 25-JAN-2001.
PA (RESC-) UNIV CALIFORNIA.
Query Match 22.0%; Score 199.8; DB 4; Length 160552;
Best Local Similarity 76.7%; Pred. No. 4.9e-46;
RESULT 712
ID ABD33314 standard; DNA; 170489 BP.
DE Human cancer-associated (CA) gene HD07-056.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.8; DB 13; Length 170489;
Best Local Similarity 80.9%; Pred. No. 5.1e-46;
RESULT 713
ID ACN43946 standard; DNA; 174448 BP.
DE Human genomic sequence hCG21793.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.8; DB 11; Length 174448;
Best Local Similarity 82.0%; Pred. No. 5.1e-46;
RESULT 714
ID ADE09750 standard; DNA; 1608 BP.
DE Novel DNA-related contig nucleotide sequence #472.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.6; DB 10; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 715
ID ADS11591 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1828.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 716
ID ADS11592 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1829.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 717
ID ADS11590 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1827.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 718
ID ADS11159 standard; DNA; 1608 BP.
DE Human therapeutic contig DNA - SEQ ID 1396.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 1608;
Best Local Similarity 84.1%; Pred. No. 9.6e-47;
RESULT 719
ID AAK94819 standard; cDNA; 1748 BP.
DE Human full-length cDNA, SEQ ID NO: 3960.
PN EP130084-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 22.0%; Score 199.6; DB 4; Length 1748;
Best Local Similarity 84.1%; Pred. No. 9.9e-47;
RESULT 720
ID AD131927 standard; cDNA; 1748 BP.
DE Full length human cDNA clone Seqid 3960.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.0%; Score 199.6; DB 12; Length 1748;
Best Local Similarity 84.1%; Pred. No. 9.9e-47;
RESULT 721
ID ADA52479 standard; cDNA; 2261 BP.
DE Human coding sequence, SEQ ID 47.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
Query Match 22.0%; Score 199.6; DB 10; Length 2261;
Best Local Similarity 84.1%; Pred. No. 1.1e-46;
RESULT 722
ID AAI59666 standard; cDNA; 2982 BP.
DE Human polynucleotide SEQ ID NO 3655.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.6; DB 4; Length 2982;
Best Local Similarity 84.1%; Pred. No. 1.2e-46;
RESULT 723
ID ABK69113 standard; cDNA; 3047 BP.
DE DNA encoding human secreted protein, SEQ ID NO 37.
PN WO200224721-A1.
PD 28-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 6; Length 3047;
Best Local Similarity 84.1%; Pred. No. 1.2e-46;
RESULT 724
ID AAI57880 standard; cDNA; 3262 BP.
DE Human polynucleotide SEQ ID NO 83.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 22.0%; Score 199.6; DB 4; Length 3262;
Best Local Similarity 84.1%; Pred. No. 1.3e-46;
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RESULT 725
ID ADQ67504 standard; cDNA; 3660 BP.
DE Novel human cDNA sequence #2477.
PN EPI440981-A2.
PD 28-JUL-2004.
PA (REMS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.0%; Score 199.6; DB 12; Length 3660;
Best Local Similarity 84.1%; Pred. No. 1.3e-46;
RESULT 726
ID ABQ75955 standard; cDNA; 3716 BP.
DE Human PPMV encoding sequence Incyte ID 7972712CB1.
PN WO200246383-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.0%; Score 199.6; DB 6; Length 3716;
Best Local Similarity 84.1%; Pred. No. 1.3e-46;
RESULT 727
ID ABK83341 standard; cDNA; 4037 BP.
DE cDNA encoding human DDRP-2 splice variant #9.
PN WO200231134-A2.
PD 18-APR-2002.
PA (FERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4037;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 728
ID ABK83337 standard; cDNA; 4076 BP.
DE cDNA encoding human DDRP-2 splice variant #5.
PN WO200231134-A2.
PD 18-APR-2002.
PA (FERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4076;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 729
ID ABK83340 standard; cDNA; 4120 BP.
DE cDNA encoding human DDRP-2 splice variant #8.
PN WO200231134-A2.
PD 18-APR-2002.
PA (FERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4120;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 730
ID ADQ86753 standard; cDNA; 4147 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3628.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WUTD-) WU T D.
PA (ZHOU-) ZHOU Y.
Query Match 22.0%; Score 199.6; DB 12; Length 4147;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 731
ID ADQ84273 standard; cDNA; 4147 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1087.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH-) GENENTECH INC.
PA (WUTD-) WU T D.
PA (ZHOU-) ZHOU Y.
Query Match 22.0%; Score 199.6; DB 13; Length 4147;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 732
ID ACN440423 standard; cDNA; 4147 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA26538, SEQ ID NO:5194.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 22.0%; Score 199.6; DB 13; Length 4147;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 733
ID ABK83336 standard; cDNA; 4159 BP.
DE cDNA encoding human DDRP-2 splice variant #4.
PN WO200231134-A2.
PD 18-APR-2002.

PA (FERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4159;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 734
ID ABK83339 standard; cDNA; 4180 BP.
DE cDNA encoding human DDRP-2 splice variant #7.
PN WO200231134-A2.
PD 18-APR-2002.
PA (FERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4180;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 735
ID ABK83335 standard; cDNA; 4219 BP.
DE cDNA encoding human DDRP-2 splice variant #3.
PN WO200231134-A2.
PD 18-APR-2002.
PA (FERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4219;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 736
ID ABK83338 standard; cDNA; 4263 BP.
DE cDNA encoding human DDRP-2 splice variant #6.
PN WO200231134-A2.
PD 18-APR-2002.
PA (FERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4263;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 737
ID ADS10268 standard; DNA; 4284 BP.
DE Human therapeutic DNA - SEQ ID 505.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 4284;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 738
ID ABK83333 standard; cDNA; 4302 BP.
DE cDNA encoding human DDRP-2 splice variant #1.
PN WO200231134-A2.
PD 18-APR-2002.
PA (FERR-) FERRING BV.
Query Match 22.0%; Score 199.6; DB 6; Length 4302;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 739
ID ADS10269 standard; DNA; 4359 BP.
DE Human therapeutic DNA - SEQ ID 506.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 4359;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 740
ID ADS10267 standard; DNA; 4398 BP.
DE Human therapeutic DNA - SEQ ID 504.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 22.0%; Score 199.6; DB 13; Length 4398;
Best Local Similarity 84.1%; Pred. No. 1.4e-46;
RESULT 741
ID AAK79131 standard; DNA; 14216 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33943.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 4; Length 14216;
Best Local Similarity 84.1%; Pred. No. 2.2e-46;
RESULT 742
ID AAK79133 standard; DNA; 14216 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33945.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 22.0%; Score 199.6; DB 4; Length 14216;
Best Local Similarity 84.1%; Pred. No. 2.2e-46;
RESULT 743
ID AAS41759 standard; DNA; 22428 BP.
DE Genomic sequence #75 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 4; Length 22428;
Best Local Similarity 84.1%; Pred. No. 2.6e-46;
RESULT 744
ID ABZ74201 standard; DNA; 22428 BP.
DE Secreted protein gene 215 genomic fragment HNGAMS8, SEQ ID NO:1348.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 8; Length 22428;
Best Local Similarity 84.1%; Pred. No. 2.6e-46;
RESULT 745
ID ADA98730 standard; DNA; 22428 BP.
DE Human secreted protein-related DNA sequence #323.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 8; Length 22428;
Best Local Similarity 84.1%; Pred. No. 2.6e-46;
RESULT 746
ID ABZ6767 standard; DNA; 22428 BP.
DE Human secreted protein encoding genomic DNA SEQ ID NO 1290.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 10; Length 22428;
Best Local Similarity 84.1%; Pred. No. 2.6e-46;
RESULT 747
ID AAK81763 standard; DNA; 37959 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36575.
PN WO200157183-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.6; DB 4; Length 37959;
Best Local Similarity 82.8%; Pred. No. 3.2e-46;
RESULT 748
ID ACN44818 standard; DNA; 116704 BP.
DE Human genomic sequence hCG30155.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.6; DB 11; Length 116704;
Best Local Similarity 82.9%; Pred. No. 5e-46;
RESULT 749
ID ADP60536 standard; DNA; 118788 BP.
DE Human HPC2/ELAC2 gene SeqID1.
PN JP200416565-A.
PD 17-JUN-2004.
PA (TAKA/) TAKAHASHI H.
PA (WATA/) WATANABE M.
PA (FURU/) FURUSATO M.
PA (HONS) YAKULT HONSHA KK.
Query Match 22.0%; Score 199.6; DB 12; Length 118788;
Best Local Similarity 82.8%; Pred. No. 5e-46;
RESULT 750
ID ABD33219 standard; DNA; 135827 BP.
DE Human cancer-associated (CA) gene HD07-035.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.6; DB 13; Length 135827;
Best Local Similarity 78.6%; Pred. No. 5.3e-46;
RESULT 751
ID ABD32612 standard; DNA; 142976 BP.
DE Human cancer-associated genomic DNA HD12-017.
PN WO2004074320-A2.

PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.6; DB 13; Length 142976;
Best Local Similarity 83.1%; Pred. No. 5.4e-46;
RESULT 752
ID ACN44374 standard; DNA; 181684 BP.
DE Human genomic sequence hCG16651.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.6; DB 11; Length 181684;
Best Local Similarity 82.8%; Pred. No. 5.9e-46;
RESULT 753
ID AAH92610 standard; DNA; 700 BP.
DE Human inflammatory bowel disease related gene fragment IGR1310a.
PN WO200142511-A2.
PD 14-JUN-2001.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (ELIT-) ELIIPSIS BIOTHERAPEUTICS CORP.
Query Match 22.0%; Score 199.4; DB 4; Length 700;
Best Local Similarity 81.1%; Pred. No. 7.9e-47;
RESULT 754
ID AAL36476 standard; DNA; 1664 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2841.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.4; DB 4; Length 1664;
Best Local Similarity 86.4%; Pred. No. 1.1e-46;
RESULT 755
ID ABX59464 standard; CDNA; 1664 BP.
DE CDNA encoding novel human musculoskeletal system antigen #1808.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.0%; Score 199.4; DB 8; Length 1664;
Best Local Similarity 86.4%; Pred. No. 1.1e-46;
RESULT 756
ID ADJ30214 standard; DNA; 1664 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2841.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.4; DB 12; Length 1664;
Best Local Similarity 86.4%; Pred. No. 1.1e-46;
RESULT 757
ID ADM03474 standard; CDNA; 1756 BP.
DE Human CDNA of the invention SEQ ID NO:2159.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 22.0%; Score 199.4; DB 11; Length 1756;
Best Local Similarity 82.4%; Pred. No. 1.1e-46;
RESULT 758
ID ABK92513 standard; DNA; 6096 BP.
DE Human prostate specific nucleic acid #132.
PN WO200238810-A2.
PD 16-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 22.0%; Score 199.4; DB 6; Length 6096;
Best Local Similarity 76.0%; Pred. No. 1.8e-46;
RESULT 759
ID AAS42014 standard; DNA; 6437 BP.
DE Genomic sequence #330 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.4; DB 4; Length 6437;
Best Local Similarity 81.1%; Pred. No. 1.9e-46;
RESULT 760
ID AAK69231 standard; DNA; 8658 BP.

DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24043.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.4; DB 4; Length 8658;
Best Local Similarity 81.1%; Pred. No. 2.1e-46;
RESULT 761
ID AAS42015 standard; DNA; 9742 BP.
DE Genomic sequence #331 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.4; DB 4; Length 9742;
Best Local Similarity 81.1%; Pred. No. 2.2e-46;
RESULT 762
ID ACN44990 standard; DNA; 33317 BP.
DE Human genomic sequence hccg27461.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.4; DB 11; Length 33317;
Best Local Similarity 81.3%; Pred. No. 3.5e-46;
RESULT 763
ID AAD44995 standard; DNA; 49984 BP.
DE Human transporter genomic DNA.
Query Match 22.0%; Score 199.4; DB 6; Length 49984;
Best Local Similarity 81.1%; Pred. No. 4.1e-46;
RESULT 764
ID ADS64392 standard; DNA; 49984 BP.
DE Human transporter protein encoding gene.
Query Match 22.0%; Score 199.4; DB 13; Length 49984;
Best Local Similarity 81.1%; Pred. No. 4.1e-46;
RESULT 765
ID AAL53466 standard; DNA; 70372 BP.
DE Ras-like protein genomic DNA.
Query Match 22.0%; Score 199.4; DB 6; Length 70372;
Best Local Similarity 81.1%; Pred. No. 4.7e-46;
RESULT 766
ID ADQ97870 standard; DNA; 121160 BP.
DE Human cancer associated sequence HD11-015, SEQ ID 847.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.4; DB 12; Length 121160;
Best Local Similarity 76.0%; Pred. No. 5.8e-46;
RESULT 767
ID ADH19244 standard; DNA; 124164 BP.
DE Human 5-hydroxytryptamine receptor type 3B SNP variant DNA.
PN WO2003097873-A2.
PD 27-NOV-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.0%; Score 199.4; DB 12; Length 124164;
Best Local Similarity 81.1%; Pred. No. 5.8e-46;
RESULT 768
ID ADH19246 standard; DNA; 124165 BP.
DE Human 5-hydroxytryptamine receptor type 3B SNP variant DNA 2.
PN WO2003097873-A2.
PD 27-NOV-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.0%; Score 199.4; DB 12; Length 124165;
Best Local Similarity 81.1%; Pred. No. 5.8e-46;
RESULT 769
ID ADP83402 standard; DNA; 124167 BP.
DE Human 5-hydroxytryptamine receptor type 3 gene.
PN WO2003100091-A1.
PD 04-DEC-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.0%; Score 199.4; DB 12; Length 124167;
Best Local Similarity 81.1%; Pred. No. 5.8e-46;
RESULT 770
ID ADH19240 standard; DNA; 124167 BP.
DE Human 5-hydroxytryptamine receptor type 3B gDNA.
PN WO2003097873-A2.

PD 27-NOV-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 22.0%; Score 199.4; DB 12; Length 124167;
Best Local Similarity 81.1%; Pred. No. 5.8e-46;
RESULT 771
ID ADQ97301 standard; DNA; 127722 BP.
DE Human cancer associated sequence HD08-028, SEQ ID 278.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.4; DB 12; Length 127722;
Best Local Similarity 81.5%; Pred. No. 5.9e-46;
RESULT 772
ID AAD5538 standard; DNA; 133893 BP.
DE Human phosphatidylinositol diphosphate (PIB) DNA #1.
PN WO200299125-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 22.0%; Score 199.4; DB 9; Length 133893;
Best Local Similarity 78.9%; Pred. No. 6e-46;
RESULT 773
ID ADL1638 standard; DNA; 186528 BP.
DE Osteoarthritis-associated polymorphic nucleotide #170.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 22.0%; Score 199.4; DB 10; Length 186528;
Best Local Similarity 79.9%; Pred. No. 6.8e-46;
RESULT 774
ID ABD32598 standard; DNA; 290547 BP.
DE Human cancer-associated genomic DNA HD7-220.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.4; DB 13; Length 290547;
Best Local Similarity 81.1%; Pred. No. 8.1e-46;
RESULT 775
ID AAX61843 standard; DNA; 601 BP.
DE Novel human transporter protein related polynucleotide #39.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KERC/) KENCHIM K A.
PA (OPRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 22.0%; Score 199.2; DB 8; Length 601;
Best Local Similarity 76.7%; Pred. No. 8.5e-47;
RESULT 776
ID AAK80126 standard; DNA; 4115 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34938.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.2; DB 4; Length 4115;
Best Local Similarity 84.6%; Pred. No. 1.8e-46;
RESULT 777
ID ABQ78002 standard; DNA; 21222 BP.
DE Human transporter protein encoding genomic DNA SEQ ID NO 3.
Query Match 22.0%; Score 199.2; DB 6; Length 21222;
Best Local Similarity 80.6%; Pred. No. 3.4e-46;
RESULT 778
ID AAK89418 standard; DNA; 28588 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2994.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.2; DB 4; Length 28588;
Best Local Similarity 82.8%; Pred. No. 3.6e-46;
RESULT 779
ID AAS31923 standard; DNA; 28588 BP.
DE Human liver associated genomic DNA #97.
PN WO200155355-A1.
PD 02-AUG-2001.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.2; DB 5; Length 28588;
Best Local Similarity 82.8%; Pred. No. 3.8e-46;
RESULT 780
ID ABR90278 standard; DNA; 28588 BP.
DE Human liver antigen HMDR194 genomic sequence, SEQ ID NO:399.
PN US2002042096-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 22.0%; Score 199.2; DB 6; Length 28588;
Best Local Similarity 82.8%; Pred. No. 3.8e-46;
RESULT 781
ID ADJ15191 standard; DNA; 28588 BP.
DE Human liver-related genomic DNA - SEQ ID 399.
PN US2003077602-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 22.0%; Score 199.2; DB 11; Length 28588;
Best Local Similarity 82.8%; Pred. No. 3.8e-46;
RESULT 782
ID ABR87217 standard; DNA; 30709 BP.
DE Human lipase, hormone-sensitive (LIPF) gene sequence.
Query Match 22.0%; Score 199.2; DB 6; Length 30709;
Best Local Similarity 83.0%; Pred. No. 3.9e-46;
RESULT 783
ID ABD3578 standard; DNA; 43853 BP.
DE Human cancer-associated (CA) gene HD07-116.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.2; DB 13; Length 43853;
Best Local Similarity 80.6%; Pred. No. 4.5e-46;
RESULT 784
ID ACN4386 standard; DNA; 61103 BP.
DE Human genomic sequence hCG1784975.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.2; DB 11; Length 61103;
Best Local Similarity 81.9%; Pred. No. 5.1e-46;
RESULT 785
ID ACN44230 standard; DNA; 66973 BP.
DE Human genomic sequence hCG21559.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.2; DB 11; Length 66973;
Best Local Similarity 84.4%; Pred. No. 5.2e-46;
RESULT 786
ID ADQ97968 standard; DNA; 78082 BP.
DE Human cancer associated sequence HD11-032, SEQ ID 945.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 22.0%; Score 199.2; DB 12; Length 78082;
Best Local Similarity 82.8%; Pred. No. 5.6e-46;
RESULT 787
Query Match 22.0%; Score 199.2; DB 13; Length 88759;
Best Local Similarity 80.1%; Pred. No. 5.8e-46;
RESULT 788
ID ADH56439 standard; DNA; 95001 BP.
DE Human hypothetical tumour endothelial marker DNA.
PN US2003232770-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 22.0%; Score 199.2; DB 12; Length 95001;
Best Local Similarity 80.6%; Pred. No. 6e-46;
RESULT 789
ID ADC85301 standard; DNA; 96591 BP.
DE Mouse Sosl coding sequence.
PN WO2003045230-A2.

PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.2; DB 10; Length 96591;
Best Local Similarity 76.0%; Pred. No. 6e-46;
RESULT 790
ID ADA02822 standard; DNA; 96592 BP.
DE Human Sosl carcinoma associated gene, SEQ ID NO:1340.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.2; DB 9; Length 96592;
Best Local Similarity 76.0%; Pred. No. 6e-46;
RESULT 791
ID ADB72560 standard; DNA; 96592 BP.
DE Human Sosl gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 22.0%; Score 199.2; DB 10; Length 96592;
Best Local Similarity 76.0%; Pred. No. 6e-46;
RESULT 792
ID ADM74417 standard; DNA; 96592 BP.
DE Human carcinoma associated (CA) nucleic acid #43.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORE/) MORRIS D W.
PA (ENSE/) ENGELHARD E K.
Query Match 22.0%; Score 199.2; DB 12; Length 96592;
Best Local Similarity 76.0%; Pred. No. 6e-46;
RESULT 793
ID ADS36461 standard; DNA; 158417 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1675.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 22.0%; Score 199.2; DB 13; Length 158417;
Best Local Similarity 85.1%; Pred. No. 7.3e-46;
RESULT 794
ID AAH13291 standard; cDNA; 559 BP.
DE Human cDNA clone (3'-primer) SEQ ID NO:10126.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 21.9%; Score 199; DB 4; Length 559;
Best Local Similarity 83.8%; Pred. No. 9.5e-47;
RESULT 795
ID AAK72518 standard; DNA; 2502 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27330.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 199; DB 4; Length 2502;
Best Local Similarity 85.1%; Pred. No. 1.7e-46;
RESULT 796
ID AAK70822 standard; DNA; 3371 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25634.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 199; DB 4; Length 3371;
Best Local Similarity 78.0%; Pred. No. 1.9e-46;
RESULT 797
ID ADQ64845 standard; cDNA; 4634 BP.
DE Novel human cDNA sequence #2006.
PN EP1440981-A2.
PD 28-JUL-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.9%; Score 199; DB 12; Length 4634;
Best Local Similarity 85.1%; Pred. No. 2.1e-46;
RESULT 798
ID ABA20857 standard; DNA; 11234 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13188.
PN WO200159063-A2.

PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 199; DB 5; Length 11234;
Best Local Similarity 81.3%; Pred. No. 3e-46;
RESULT 799
ID ABK49701 standard; DNA; 32816 BP.
DE Human transporter protein genomic DNA sequence.
Query Match 21.9%; Score 199; DB 6; Length 32816;
Best Local Similarity 85.1%; Pred. No. 4.5e-46;
RESULT 800
ID ADG16994 standard; DNA; 32816 BP.
DE Human transporter protein DNA.
Query Match 21.9%; Score 199; DB 12; Length 32816;
Best Local Similarity 85.1%; Pred. No. 4.5e-46;
RESULT 801
ID ABX13675 standard; DNA; 33239 BP.
DE Human secreted protein gene.
PN US2002137130-A1.
PD 26-SEP-2002.
PA (WEIM/) WEI M.
PA (GONG/) GONG F.
PA (DEPA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 21.9%; Score 199; DB 8; Length 33239;
Best Local Similarity 81.5%; Pred. No. 4.6e-46;
RESULT 802
ID AAK74751 standard; DNA; 36485 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:29563.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 199; DB 4; Length 36485;
Best Local Similarity 80.1%; Pred. No. 4.7e-46;
RESULT 803
ID AAK68958 standard; DNA; 36485 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23770.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 199; DB 4; Length 36485;
Best Local Similarity 80.1%; Pred. No. 4.7e-46;
RESULT 804
ID AAD48290 standard; DNA; 39982 BP.
DE Human enzyme protein encoding gene.
Query Match 21.9%; Score 199; DB 8; Length 39982;
Best Local Similarity 85.1%; Pred. No. 4.9e-46;
RESULT 805
ID ABD32585 standard; DNA; 50927 BP.
DE Human cancer-associated genomic DNA HD7-210.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 199; DB 13; Length 50927;
Best Local Similarity 85.1%; Pred. No. 5.4e-46;
RESULT 806
ID ADO97599 standard; DNA; 106130 BP.
DE Human cancer associated sequence HD10-012, SEQ ID 576.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 199; DB 12; Length 106130;
Best Local Similarity 85.1%; Pred. No. 7.1e-46;
RESULT 807
Query Match 21.9%; Score 199; DB 11; Length 110000;
Best Local Similarity 85.1%; Pred. No. 7.2e-46;
RESULT 808
ID ACN44602 standard; DNA; 126266 BP.
DE Human genomic sequence hCG1781402.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 199; DB 11; Length 126266;
Best Local Similarity 81.5%; Pred. No. 7.6e-46;

RESULT 809
ID ADH63063 standard; DNA; 132762 BP.
DE Human fibroblast growth factor receptor 2 related sequence, SEQ ID 17.
PN WO2003024987-A1.
PD 27-MAR-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.9%; Score 199; DB 10; Length 132762;
Best Local Similarity 81.5%; Pred. No. 7.8e-46;
RESULT 810
ID ADP45594 standard; DNA; 133100 BP.
DE Human NTMNA1/FLJ20625/LOC220074 region gDNA.
Query Match 21.9%; Score 199; DB 12; Length 133100;
Best Local Similarity 81.5%; Pred. No. 7.8e-46;
RESULT 811
ID ACA62841 standard; DNA; 148567 BP.
DE Human kinase DNA.
Query Match 21.9%; Score 199; DB 9; Length 148567;
Best Local Similarity 79.3%; Pred. No. 8.1e-46;
RESULT 812
ID ABS55500 standard; DNA; 148567 BP.
DE Gene encoding human serine/threonine protein kinase-like kinase.
Query Match 21.9%; Score 199; DB 10; Length 148567;
Best Local Similarity 79.3%; Pred. No. 8.1e-46;
RESULT 813
ID ADL09163 standard; DNA; 148567 BP.
DE Human protein kinase, genomic DNA.
Query Match 21.9%; Score 199; DB 12; Length 148567;
Best Local Similarity 79.3%; Pred. No. 8.1e-46;
RESULT 814
ID ACP62741 standard; DNA; 189013 BP.
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:669.
PN WO2003013534-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 21.9%; Score 199; DB 8; Length 189013;
Best Local Similarity 82.6%; Pred. No. 8.9e-46;
RESULT 815
ID ADB20856 standard; DNA; 189013 BP.
DE MRP1 based cancer related nucleic acid SEQ ID NO:669.
PN WO2003013533-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 21.9%; Score 199; DB 8; Length 189013;
Best Local Similarity 82.6%; Pred. No. 8.9e-46;
RESULT 816
ID ADB87945 standard; DNA; 189013 BP.
DE Human UGT1A1 gene sequence SEQ ID NO:669.
PN WO2003013536-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 21.9%; Score 199; DB 10; Length 189013;
Best Local Similarity 82.6%; Pred. No. 8.9e-46;
RESULT 817
ID ADB96928 standard; DNA; 189013 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:669.
PN WO2003013537-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 21.9%; Score 199; DB 10; Length 189013;
Best Local Similarity 82.6%; Pred. No. 8.9e-46;
RESULT 818
ID ADB92119 standard; DNA; 189013 BP.
DE Human MDR1 related DNA sequence SEQ ID NO:669.
PN WO2003013535-A2.
PD 20-FEB-2003.
PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
Query Match 21.9%; Score 199; DB 10; Length 189013;
Best Local Similarity 82.6%; Pred. No. 8.9e-46;
RESULT 819
ID ACN44170 standard; DNA; 196686 BP.
DE Human genomic sequence hCG39530.
PN WO2003073826-A2.
PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 199; DB 11; Length 196686;
Best Local Similarity 81.3%; Pred. No. 9.1e-46;
RESULT 820
ID ADC86916 standard; DNA; 349989 BP.
DE Human GPCR gene SEQ ID NO:1369.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (MAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 21.9%; Score 199; DB 10; Length 349989;
Best Local Similarity 78.5%; Pred. No. 1.1e-45;
RESULT 821
ID ABN62834 standard; cDNA; 402 BP.
DE Human cancer related polynucleotide SEQ ID NO 2801.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR-) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match 21.9%; Score 198.8; DB 6; Length 402;
Best Local Similarity 79.6%; Pred. No. 9.5e-47;
RESULT 822
ID AAK75637 standard; DNA; 2173 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30449.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 2173;
Best Local Similarity 75.2%; Pred. No. 1.8e-46;
RESULT 823
ID AAH16224 standard; cDNA; 2591 BP.
DE Human cDNA sequence SEQ ID NO:15042.
PN EPI074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 21.9%; Score 198.8; DB 4; Length 2591;
Best Local Similarity 81.8%; Pred. No. 2e-46;
RESULT 824
ID ADL22885 standard; DNA; 2591 BP.
DE Human WP2153 coding sequence SEQ ID NO: 5.
PN WO2004015069-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Query Match 21.9%; Score 198.8; DB 12; Length 2591;
Best Local Similarity 81.8%; Pred. No. 2e-46;
RESULT 825
ID ADRI4082 standard; DNA; 2591 BP.
DE Human NF-kappaB pathway-associated gene SeqID83.
PN WO2004065577-A2.
PD 05-AUG-2004.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
Query Match 21.9%; Score 198.8; DB 13; Length 2591;
Best Local Similarity 81.8%; Pred. No. 2e-46;
RESULT 826
ID ADRO8024 standard; cDNA; 3385 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1530.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.9%; Score 198.8; DB 13; Length 3385;
Best Local Similarity 85.9%; Pred. No. 2.2e-46;
RESULT 827
ID ACN37218 standard; DNA; 20001 BP.
DE Human periodontal disease related gene PTCDS SEQ ID NO:128.
PN WO2004042054-A1.
PD 21-MAY-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (KAMC/) KAMOI K.
Query Match 21.9%; Score 198.8; DB 13; Length 20001;
Best Local Similarity 83.0%; Pred. No. 4.3e-46;
RESULT 828
ID AAK81266 standard; DNA; 21458 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36078.

PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 21458;
Best Local Similarity 82.1%; Pred. No. 4.4e-46;
RESULT 829
ID AAL06122 standard; DNA; 21458 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8810.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 21458;
Best Local Similarity 82.1%; Pred. No. 4.4e-46;
RESULT 830
ID ABL98687 standard; DNA; 21458 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3339.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 21458;
Best Local Similarity 82.1%; Pred. No. 4.4e-46;
RESULT 831
ID ABK42270 standard; DNA; 21470 BP.
DE Genomic sequence #169 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 21470;
Best Local Similarity 83.0%; Pred. No. 4.4e-46;
RESULT 832
ID ADB60426 standard; DNA; 21470 BP.
DE Connective tissue related genomic DNA #169.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 9; Length 21470;
Best Local Similarity 83.0%; Pred. No. 4.4e-46;
RESULT 833
ID ADA02702 standard; DNA; 21666 BP.
DE Human Nuprl carcinoma associated gene, SEQ ID NO:1220.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.8; DB 9; Length 21666;
Best Local Similarity 84.9%; Pred. No. 4.4e-46;
RESULT 834
ID ADB72440 standard; DNA; 21666 BP.
DE Human CA gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.8; DB 10; Length 21666;
Best Local Similarity 84.9%; Pred. No. 4.4e-46;
RESULT 835
ID ADB95950 standard; DNA; 21666 BP.
DE Human hCG1745228 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.8; DB 10; Length 21666;
Best Local Similarity 84.9%; Pred. No. 4.4e-46;
RESULT 836
ID ADK40307 standard; DNA; 23469 BP.
DE Human HNF1alpha gene SEQ ID NO:27.
PN WO2004016813-A2.
PD 26-FEB-2004.
PA (INEM-) INSERM INST NAT SANTE & RECH MEDICALE.
Query Match 21.9%; Score 198.8; DB 12; Length 23469;
Best Local Similarity 77.3%; Pred. No. 4.6e-46;
RESULT 837
ID ACN37244 standard; DNA; 25382 BP.
DE Human periodontal disease related gene IL4R SEQ ID NO:154.
Query Match 21.9%; Score 198.8; DB 13; Length 25382;

Best Local Similarity 82.1%; Pred. No. 4.7e-46;
RESULT 838
ID AAF57718 standard; DNA; 28690 BP.
DE Human IL4RaIpha gene.
PN WO200104270-A1.
PD 18-JAN-2001.
PA (GENA-) GENMISANCE PHARM INC.
Query Match 21.9%; Score 198.8; DB 5; Length 28690;
Best Local Similarity 82.1%; Pred. No. 4.9e-46;
RESULT 839
ID ADS36474 standard; DNA; 40947 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1688.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 21.9%; Score 198.8; DB 13; Length 40947;
Best Local Similarity 79.7%; Pred. No. 5.7e-46;
RESULT 840
ID AAK6531 standard; DNA; 41159 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20443.
PN 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.8; DB 4; Length 41159;
Best Local Similarity 81.2%; Pred. No. 5.7e-46;
RESULT 841
ID AAD36022 standard; DNA; 43950 BP.
DE Human kinase genomic DNA.
Query Match 21.9%; Score 198.8; DB 6; Length 43950;
Best Local Similarity 81.2%; Pred. No. 5.8e-46;
RESULT 842
ID ABD33486 standard; DNA; 51289 BP.
DE Human cancer-associated (CA) gene HD07-094.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.8; DB 13; Length 51289;
Best Local Similarity 86.2%; Pred. No. 6.2e-46;
RESULT 843
ID ABD33339 standard; DNA; 62658 BP.
DE Human cancer-associated (CA) gene HD07-061.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.8; DB 13; Length 62658;
Best Local Similarity 81.2%; Pred. No. 6.7e-46;
RESULT 844
ID ACN44522 standard; DNA; 70779 BP.
DE Human genomic sequence hCG17357.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.8; DB 11; Length 70779;
Best Local Similarity 82.1%; Pred. No. 7e-46;
RESULT 845
ID ABI64158 standard; DNA; 84539 BP.
DE Stomach cancer related gene sequence SEQ ID NO:2495.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 21.9%; Score 198.8; DB 6; Length 84539;
Best Local Similarity 75.6%; Pred. No. 7.5e-46;
RESULT 846
ID ADL13479 standard; DNA; 84539 BP.
DE Osteoarthritis-associated polymorphic nucleotide #11.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.9%; Score 198.8; DB 10; Length 84539;
Best Local Similarity 75.6%; Pred. No. 7.5e-46;
RESULT 847
ID ADM29048 standard; DNA; 130020 BP.
DE Human interleukin 4 receptor (IL4R) genomic DNA SEQ ID NO:88.
PN EPI405921-A1.
PD 07-APR-2004.
PA (HOFF) ROCHE DIAGNOSTICS GMBH.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
Query Match 21.9%; Score 198.8; DB 12; Length 130020;
Best Local Similarity 82.1%; Pred. No. 8.8e-46;
RESULT 848
ID ACN44070 standard; DNA; 344548 BP.
DE Human genomic sequence hCG35954.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.8; DB 11; Length 344548;
Best Local Similarity 83.3%; Pred. No. 1.3e-45;
RESULT 849
ID ADQ97146 standard; DNA; 348101 BP.
DE Human cancer associated sequence HD08-007, SEQ ID 122.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.8; DB 12; Length 348101;
Best Local Similarity 82.1%; Pred. No. 1.3e-45;
RESULT 850
ID AAG52592 standard; cDNA; 1191 BP.
DE cDNA sequence #379 encoding novel human secreted protein.
PN WO200177291-A2.
PD 18-OCT-2001.
PA (GEMY) GENETICS INST INC.
Query Match 21.9%; Score 198.6; DB 6; Length 1191;
Best Local Similarity 85.4%; Pred. No. 1.7e-46;
RESULT 851
ID AAI58575 standard; cDNA; 1946 BP.
DE Human polynucleotide SEQ ID NO 778.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 21.9%; Score 198.6; DB 4; Length 1946;
Best Local Similarity 82.8%; Pred. No. 2e-46;
RESULT 852
ID ADQ98792 standard; cDNA; 1946 BP.
DE DNA encoding human GPCR-like protein seqid 462.
PN US6569662-B1.
PD 27-MAY-2003.
PA (HYSE-) HYSEQ INC.
Query Match 21.9%; Score 198.6; DB 5; Length 1946;
Best Local Similarity 82.8%; Pred. No. 2e-46;
RESULT 853
ID ADB48552 standard; cDNA; 1946 BP.
DE Novel human cDNA SEQ ID NO 462.
PN US2003104529-A1.
PD 05-JUN-2003.
PA (ZHOU/) ZHOU P.
PA (TANG/) TANG Y T.
PA (LIUC/) LIU C.
PA (ASUN/) ASUNDI V.
PA (DRMA/) DRMANAC R T.
Query Match 21.9%; Score 198.6; DB 9; Length 1946;
Best Local Similarity 82.8%; Pred. No. 2e-46;
RESULT 854
ID AAK83412 standard; DNA; 4156 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38224.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 4156;
Best Local Similarity 80.3%; Pred. No. 2.7e-46;
RESULT 855
ID AAK6667 standard; DNA; 4963 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23479.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 4963;

Best Local Similarity 80.3%; Pred. No. 2.9e-46;
RESULT 856
ID AAL6538 standard; DNA; 4963 BP.
DE Human musculoskeletal system related polynucleotide SEQ ID NO 2903.
PN WO200155367-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 4963;
Best Local Similarity 80.3%; Pred. No. 2.9e-46;
RESULT 857
ID ABX59526 standard; cDNA; 4963 BP.
DE cDNA encoding novel human musculoskeletal system antigen #1870.
PN US2002147140-A1.
PD 10-OCT-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.9%; Score 198.6; DB 8; Length 4963;
Best Local Similarity 80.3%; Pred. No. 2.9e-46;
RESULT 858
ID ADJ30276 standard; DNA; 4963 BP.
DE Human musculoskeletal system-associated genomic DNA - SEQ ID 2903.
PN US2004009488-A1.
PD 15-JAN-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 12; Length 4963;
Best Local Similarity 80.3%; Pred. No. 2.9e-46;
RESULT 859
ID ADR06579 standard; cDNA; 5840 BP.
DE Full length human cDNA useful for treating neurological disease Seq 85.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.9%; Score 198.6; DB 13; Length 5840;
Best Local Similarity 82.8%; Pred. No. 3e-46;
RESULT 860
ID AAS26766 standard; DNA; 6096 BP.
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1740.
PN WO200135322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 6096;
Best Local Similarity 77.7%; Pred. No. 3.1e-46;
RESULT 861
ID ABX74115 standard; DNA; 6096 BP.
DE Human novel polynucleotide #943.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.9%; Score 198.6; DB 8; Length 6096;
Best Local Similarity 77.7%; Pred. No. 3.1e-46;
RESULT 862
ID ABK64514 standard; cDNA; 12263 BP.
DE Human cDNA differentially expressed in granulocytic cells #1085.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.9%; Score 198.6; DB 6; Length 12263;
Best Local Similarity 80.8%; Pred. No. 4.1e-46;
RESULT 863
ID ABA94501 standard; DNA; 15297 BP.
DE Human proto-oncogene tyrosine kinase genomic DNA sequence.
PN US6340584-B1.
PD 22-JAN-2002.
PA (PEKE) PE CORP NY.
Query Match 21.9%; Score 198.6; DB 6; Length 15297;
Best Local Similarity 80.8%; Pred. No. 4.4e-46;
RESULT 864
ID ABV75414 standard; DNA; 15297 BP.
DE Human kinase genomic DNA sequence.
PN WO200277191-A2.
PD 03-OCT-2002.
PA (PEKE) PE CORP NY.
Query Match 21.9%; Score 198.6; DB 8; Length 15297;
Best Local Similarity 80.8%; Pred. No. 4.4e-46;
RESULT 865
ID ADM28582 standard; cDNA; 15297 BP.
DE Human proto-oncogene tyrosine kinase DNA.
PN US2004063130-A1.
PD 01-APR-2004.
PA (APPL-) APPLERA CORP.
Query Match 21.9%; Score 198.6; DB 12; Length 15297;
Best Local Similarity 80.8%; Pred. No. 4.4e-46;
RESULT 866
ID AAK75677 standard; DNA; 16424 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30489.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 16424;
Best Local Similarity 82.8%; Pred. No. 4.5e-46;
RESULT 867
ID AAK68448 standard; DNA; 16424 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23260.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 16424;
Best Local Similarity 82.8%; Pred. No. 4.5e-46;
RESULT 868
ID ABA08132 standard; DNA; 32152 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 927.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 32152;
Best Local Similarity 74.8%; Pred. No. 5.9e-46;
RESULT 869
ID ADP75184 standard; DNA; 35192 BP.
DE Human ADAM19 gene fragment #4.
PN WO2003031594-A2.
PD 17-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 21.9%; Score 198.6; DB 11; Length 35192;
Best Local Similarity 82.8%; Pred. No. 6.1e-46;
RESULT 870
ID ADQ97084 standard; DNA; 38690 BP.
DE Human cancer associated sequence HD10-004, SEQ ID 60.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.6; DB 12; Length 38690;
Best Local Similarity 82.8%; Pred. No. 6.3e-46;
RESULT 871
ID AAK78219 standard; DNA; 47090 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33031.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 47090;
Best Local Similarity 79.2%; Pred. No. 6.8e-46;
RESULT 872
ID AAK68725 standard; DNA; 47090 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23537.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.6; DB 4; Length 47090;
Best Local Similarity 79.2%; Pred. No. 6.8e-46;
RESULT 873
ID ABQ76896 standard; DNA; 53226 BP.
DE Human G-protein coupled receptor DNA SEQ ID 3.
PN US2002142951-A1.
PD 03-OCT-2002.

PA (WEBB/) WEBSTER M.
PA (BEAS/) BEASLEY E M.
PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
Query Match 21.9%; Score 198.6; DB 10; Length 53226;
Best Local Similarity 82.8%; Pred. No. 7.1e-46;
RESULT 874
ID ADJ84182 standard; DNA; 76698 BP.
DE Human c-rai genomic DNA which is a target for antisense therapy.
PN WO2004003134-A2.
PD 08-JUN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.9%; Score 198.6; DB 12; Length 76698;
Best Local Similarity 82.8%; Pred. No. 8.2e-46;
RESULT 875
ID ABO88164 standard; cDNA; 86080 BP.
DE Human osteoblast differentiation related cDNA SEQ ID NO 71.
PN WO200250301-A2.
PD 27-JUN-2002.
PA (GENE-) GENE LOGIC INC.
PA (PROC-) PROCTER & GAMBLE CO.
Query Match 21.9%; Score 198.6; DB 6; Length 86080;
Best Local Similarity 82.7%; Pred. No. 8.6e-46;
RESULT 876
ID ABR83561 standard; cDNA; 86080 BP.
DE Human cDNA differentially expressed in granulocytic cells #132.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.9%; Score 198.6; DB 6; Length 86080;
Best Local Similarity 82.7%; Pred. No. 8.6e-46;
RESULT 877
ID ADD71054 standard; DNA; 86080 BP.
DE Human protective protein for beta-galactosidase gene SEQ ID NO:58.
PN WO2003061564-A2.
PD 31-JUL-2003.
PA (GENE-) GENE LOGIC INC.
PA (IGBI-) LG BIOMEDICAL INST.
Query Match 21.9%; Score 198.6; DB 10; Length 86080;
Best Local Similarity 82.7%; Pred. No. 8.6e-46;
RESULT 878
ID ADQ18878 standard; DNA; 86080 BP.
DE Human fetal tissue sarcoma-upregulated DNA - SEQ ID 1697.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.9%; Score 198.6; DB 12; Length 86080;
Best Local Similarity 82.7%; Pred. No. 8.6e-46;
RESULT 879
ID ADL13497 standard; DNA; 91823 BP.
DE Osteoarthritis-associated polymorphic nucleotide #29.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.9%; Score 198.6; DB 10; Length 91823;
Best Local Similarity 82.7%; Pred. No. 8.8e-46;
RESULT 880
ID ACN444930 standard; DNA; 106378 BP.
DE Human genomic sequence hCG1742422.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.6; DB 11; Length 106378;
Best Local Similarity 80.3%; Pred. No. 9.3e-46;
RESULT 881
ID ADO32260 standard; DNA; 106707 BP.
DE Human chromosome 20 region containing type 2 diabetes mellitus genes.
PN WO2004039954-A2.
PD 13-MAY-2004.
PA (JOSL-) JOSLIN DIABETES CENT INC.
Query Match 21.9%; Score 198.6; DB 12; Length 106707;
Best Local Similarity 82.8%; Pred. No. 9.3e-46;
RESULT 882

Query Match 21.9%; Score 198.6; DB 10; Length 110000;
Best Local Similarity 84.1%; Pred. No. 9.4e-46;
RESULT 883
Query Match 21.9%; Score 198.6; DB 10; Length 110000;
Best Local Similarity 84.1%; Pred. No. 9.4e-46;
RESULT 884
ID ABD32861 standard; DNA; 118466 BP.
DE Human cancer-associated genomic DNA HD17-042.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.6; DB 13; Length 118466;
Best Local Similarity 82.8%; Pred. No. 9.7e-46;
RESULT 885
ID ADQ97870 standard; DNA; 121160 BP.
DE Human cancer associated sequence HD11-015. SEQ ID 847.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.6; DB 12; Length 121160;
Best Local Similarity 84.3%; Pred. No. 9.8e-46;
RESULT 886
ID ABL10719 standard; cDNA; 122748 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 853.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.9%; Score 198.6; DB 6; Length 122748;
Best Local Similarity 80.3%; Pred. No. 9.9e-46;
RESULT 887
ID ABL68213 standard; DNA; 145831 BP.
DE Prostate cancer related gene sequence SEQ ID NO:7550.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 21.9%; Score 198.6; DB 6; Length 145831;
Best Local Similarity 79.2%; Pred. No. 1.1e-45;
RESULT 888
ID ABL6806 standard; DNA; 145831 BP.
DE Lung cancer related gene sequence SEQ ID NO:5143.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 21.9%; Score 198.6; DB 6; Length 145831;
Best Local Similarity 79.2%; Pred. No. 1.1e-45;
RESULT 889
ID ABL68588 standard; DNA; 145831 BP.
DE Kidney cancer related gene sequence SEQ ID NO:6925.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 21.9%; Score 198.6; DB 6; Length 145831;
Best Local Similarity 79.2%; Pred. No. 1.1e-45;
RESULT 890
ID ABL62309 standard; DNA; 145831 BP.
DE Colon adenocarcinoma related gene sequence SEQ ID NO:646.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Query Match 21.9%; Score 198.6; DB 6; Length 145831;
Best Local Similarity 79.2%; Pred. No. 1.1e-45;
RESULT 891
ID ABL10149 standard; cDNA; 145831 BP.
DE Human breast cancer associated coding sequence SEQ ID NO: 283.
PN WO200259271-A2.
PD 01-AUG-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.9%; Score 198.6; DB 6; Length 145831;
Best Local Similarity 79.2%; Pred. No. 1.1e-45;
RESULT 892
ID AAH92378 standard; DNA; 700 BP.
DE Human inflammatory bowel disease related gene fragment IGR1078a.
PN WO200142511-A2.

PD 14-JUN-2001.
PA (WHEP) WHITEHEAD INST BIOMEDICAL RES.
PA (BLI-) ELIPISTIS BIOTHERAPEUTICS CORP.
Query Match 21.9%; Score 198.4; DB 4; Length 700;
Best Local Similarity 84.8%; Pred. No. 1.5e-46;
RESULT 893
ID ABK42296 standard; DNA; 1672 BP.
DE Genomic sequence #195 encoding novel human connective tissue polypeptide.
PN WO200155343-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.4; DB 4; Length 1672;
Best Local Similarity 81.0%; Pred. No. 2.2e-46;
RESULT 894
ID ADB60452 standard; DNA; 1672 BP.
DE Connective tissue related genomic DNA #195.
PN US2003054375-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.4; DB 9; Length 1672;
Best Local Similarity 81.0%; Pred. No. 2.2e-46;
RESULT 895
ID ADM02728 standard; cDNA; 2549 BP.
DE Human cDNA of the invention SEQ ID NO:1413.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.9%; Score 198.4; DB 11; Length 2549;
Best Local Similarity 78.8%; Pred. No. 2.5e-46;
RESULT 896
ID ABA21351 standard; DNA; 3843 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13682.
PN WO200158063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.4; DB 5; Length 3843;
Best Local Similarity 77.2%; Pred. No. 3e-46;
RESULT 897
ID AAT75298 standard; DNA; 7705 BP.
DE Nucleotide sequence encoding human RAD50 3' end.
PN WO9727284-A2.
PD 31-JUL-1997.
PA (GENE-) GENELABS TECHNOLOGIES INC.
Query Match 21.9%; Score 198.4; DB 2; Length 7705;
Best Local Similarity 84.8%; Pred. No. 3.9e-46;
RESULT 898
ID ABK86218 standard; DNA; 13919 BP.
DE DNA encoding AIP-1/FLASH promoter.
PN WO200255691-A1.
PD 18-JUL-2002.
PA (NIRK-) NIPPON KAYAKU KK.
Query Match 21.9%; Score 198.4; DB 6; Length 13919;
Best Local Similarity 78.8%; Pred. No. 4.9e-46;
RESULT 900
ID ABK86220 standard; DNA; 13919 BP.
DE AIP-1/FLASH promoter related DNA sequence #2.
PN WO200255691-A1.
PD 18-JUL-2002.
PA (NIRK-) NIPPON KAYAKU KK.
Query Match 21.9%; Score 198.4; DB 6; Length 13919;
Best Local Similarity 78.8%; Pred. No. 4.9e-46;
RESULT 901
ID ABK86229 standard; DNA; 21404 BP.
DE AIP-1/FLASH promoter related DNA sequence #3.
PN WO200255691-A1.

PD 18-JUL-2002.
PA (NIRK-) NIPPON KAYAKU KK.
Query Match 21.9%; Score 198.4; DB 6; Length 21404;
Best Local Similarity 78.8%; Pred. No. 5.7e-46;
RESULT 902
ID ADR66994 standard; DNA; 22405 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:40.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.4; DB 13; Length 22405;
Best Local Similarity 82.2%; Pred. No. 5.8e-46;
RESULT 903
ID ADS36465 standard; DNA; 25322 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1679.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 21.9%; Score 198.4; DB 13; Length 25322;
Best Local Similarity 78.8%; Pred. No. 6.1e-46;
RESULT 904
ID ADQ97189 standard; DNA; 29360 BP.
DE Human cancer associated sequence HD08-012, SEQ ID 165.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.4; DB 12; Length 29360;
Best Local Similarity 79.9%; Pred. No. 6.5e-46;
RESULT 905
ID AAK89230 standard; DNA; 30110 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 2806.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.4; DB 4; Length 30110;
Best Local Similarity 78.4%; Pred. No. 6.5e-46;
RESULT 906
ID ADS36492 standard; DNA; 34059 BP.
DE Human autoimmune disease-related genomic DNA sequence - SEQ ID 1706.
PN WO2004083403-A2.
PD 30-SEP-2004.
PA (APPL-) APPLERA CORP.
Query Match 21.9%; Score 198.4; DB 13; Length 34059;
Best Local Similarity 78.8%; Pred. No. 6.9e-46;
RESULT 907
ID AAD31198 standard; DNA; 34634 BP.
DE Human WRL-1 genomic DNA.
PN EP1209229-A1.
PD 29-MAY-2002.
PA (LESC/) LESCH K.
PA (MEYE/) MEYER J.
Query Match 21.9%; Score 198.4; DB 6; Length 34634;
Best Local Similarity 79.9%; Pred. No. 6.9e-46;
RESULT 908
ID ACN37238 standard; DNA; 48753 BP.
DE Human periodontal disease related gene HSPG2 SEQ ID NO:148.
PN WO2004082054-A1.
PD 21-MAY-2004.
PA (HUBI-) HUBIT GENOMIX INC.
PA (KAMO/) KAMOI K.
Query Match 21.9%; Score 198.4; DB 13; Length 48753;
Best Local Similarity 84.8%; Pred. No. 7.9e-46;
RESULT 909
ID ACN45166 standard; DNA; 87687 BP.
DE Human genomic sequence hCG31872.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.4; DB 11; Length 87687;
Best Local Similarity 83.0%; Pred. No. 9.9e-46;
RESULT 910
ID ADP13458 standard; DNA; 87669 BP.
DE Renal cell carcinoma differentially expressed gene #194.

PN WO2004048933-A2.
 PD 10-JUN-2004.
 PA (AMWP) TWETH.
 PA (TWIN) TWINE N C.
 PA (BURC) BURCZYNSKI M E.
 PA (TRBP) TREPICCHIO W L.
 PA (DORN) DORNER A.
 PA (STOV) STOVER J A.
 PA (SLON) SLONI D K.
 Query Match 21.9%; Score 198.4; DB 12; Length 87869;
 Best Local Similarity 82.6%; Pred. No. 9.9e-46;
 RESULT 911
 ID ACN45042 standard; DNA; 95835 BP.
 DE Human genomic sequence hCG37223.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.9%; Score 198.4; DB 11; Length 95835;
 Best Local Similarity 81.4%; Pred. No. 1e-45;
 RESULT 912
 ID ADE43582 standard; DNA; 128034 BP.
 DE Polymorphic human IDE genomic sequence, SEQ ID 187.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 PA (GENH) GEN HOSPITAL CORP.
 Query Match 21.9%; Score 198.4; DB 10; Length 128034;
 Best Local Similarity 79.6%; Pred. No. 1.1e-45;
 RESULT 913
 ID ADH54060 standard; DNA; 128034 BP.
 DE Human IDE gene variant DNA sequence SegID187.
 PN US2003224380-A1.
 PD 04-DEC-2003.
 PA (GENH) GEN HOSPITAL CORP.
 Query Match 21.9%; Score 198.4; DB 12; Length 128034;
 Best Local Similarity 79.6%; Pred. No. 1.1e-45;
 RESULT 914
 ID ABK85173 standard; cDNA; 130263 BP.
 DE Human cDNA differentially expressed in granulocytic cells #144.
 PN WO200228999-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.9%; Score 198.4; DB 6; Length 130263;
 Best Local Similarity 81.0%; Pred. No. 1.2e-45;
 RESULT 915
 ID AAL38336 standard; DNA; 143899 BP.
 DE Genomic sequence encoding a human NGR2 protein.
 PN WO200229059-A2.
 PD 11-APR-2002.
 PA (UYVA) UNIV YALE.
 PA (BIOJ) BIOGEN INC.
 Query Match 21.9%; Score 198.4; DB 6; Length 143899;
 Best Local Similarity 81.0%; Pred. No. 1.2e-45;
 RESULT 916
 ID ABL68122 standard; DNA; 174424 BP.
 DE Ovary cancer related gene sequence SEQ ID NO:6459.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 21.9%; Score 198.4; DB 6; Length 174424;
 Best Local Similarity 84.8%; Pred. No. 1.3e-45;
 RESULT 917
 ID ADQ19573 standard; DNA; 181343 BP.
 DE Human ecot tissue sarcoma-upregulated DNA - SEQ ID 2392.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.9%; Score 198.4; DB 12; Length 181343;
 Best Local Similarity 84.8%; Pred. No. 1.3e-45;
 RESULT 918
 ID ABX16034 standard; DNA; 203654 BP.
 DE Human gene encoding calcium channel transporter family member.
 PN US2002142938-A1.

PD 03-OCT-2002.
 PA (YANC) YAN C.
 PA (KETC) KETCHUM K A.
 PA (DFRA) DI FRANCESCO V.
 PA (BEAS) BEASLEY E M.
 Query Match 21.9%; Score 198.4; DB 10; Length 203654;
 Best Local Similarity 84.8%; Pred. No. 1.4e-45;
 RESULT 919
 ID ADL13471 standard; DNA; 214520 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #3.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 21.9%; Score 198.4; DB 10; Length 214520;
 Best Local Similarity 79.9%; Pred. No. 1.4e-45;
 RESULT 920
 ID AAV57926 standard; DNA; 235033 BP.
 DE Hereditary haemochromatosis subregion from an unaffected individual.
 PN WO98144466-A1.
 PD 09-APR-1998.
 PA (PROG-) PROGENITOR INC.
 Query Match 21.9%; Score 198.4; DB 2; Length 235033;
 Best Local Similarity 82.2%; Pred. No. 1.4e-45;
 RESULT 921
 ID AAK6647 standard; DNA; 598 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21459.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.9%; Score 198.2; DB 4; Length 598;
 Best Local Similarity 81.7%; Pred. No. 1.7e-46;
 RESULT 922
 ID ADQ15750 standard; DNA; 1714 BP.
 DE 4 synthesis-period of neuroblastoma related DNA, SEQ ID 12.
 PN WO2004039975-A1.
 PD 13-MAY-2004.
 PA (HISM) HISAMITSU PHARM CO LTD.
 PA (CHIB-) CHIBA PHARMACEUTICALS.
 Query Match 21.9%; Score 198.2; DB 12; Length 1714;
 Best Local Similarity 80.5%; Pred. No. 2.5e-46;
 RESULT 923
 ID ADM02856 standard; cDNA; 2062 BP.
 DE Human cDNA of the thymionin SEQ ID NO:1541.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) REAS ASSOC BIOTECHNOLOGY.
 Query Match 21.9%; Score 198.2; DB 11; Length 2062;
 Best Local Similarity 72.7%; Pred. No. 2.7e-46;
 RESULT 924
 ID ABK34800 standard; cDNA; 2541 BP.
 DE Human cDNA for novel secreted protein, SEQ ID 569.
 PN WO200177290-A2.
 PD 18-OCT-2001.
 PA (GENY) GENETICS INST INC.
 Query Match 21.9%; Score 198.2; DB 6; Length 2541;
 Best Local Similarity 82.9%; Pred. No. 2.9e-46;
 RESULT 925
 ID ABK70289 standard; cDNA; 4824 BP.
 DE Human lung cancer associated full length cDNA DMSM-59.
 PN WO200224057-A2.
 PD 28-MAR-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 21.9%; Score 198.2; DB 6; Length 4824;
 Best Local Similarity 72.7%; Pred. No. 3.7e-46;
 RESULT 926
 ID ADH28814 standard; DNA; 4824 BP.
 DE Human chronic myelogenous leukaemia (CML) gene marker #82.
 PN US2003104426-A1.
 PD 05-JUN-2003.
 PA (LINS) LINSLEY P S.
 PA (MAOM) MAO M.
 PA (DAIH) DAI H.
 PA (HEIT) HE Y.

PA (RAD1/) RAD1CH J P.
Query Match 21.9%; Score 198.2; DB 10; Length 4824;
Best Local Similarity 72.7%; Pred. No. 3.7e-46;
RESULT 927
ID ADR06591 standard; cDNA; 4865 BP.
DE Full length human cDNA useful for treating neurological disease Seq 97.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.9%; Score 198.2; DB 13; Length 4865;
Best Local Similarity 81.3%; Pred. No. 3.7e-46;
RESULT 928
ID AAS44656 standard; DNA; 4885 BP.
DE Human full-length polynucleotide sequence #81.
PN WO200164834-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 21.9%; Score 198.2; DB 4; Length 4885;
Best Local Similarity 72.7%; Pred. No. 3.7e-46;
RESULT 929
ID AAK60970 standard; DNA; 6159 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:35782.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.2; DB 4; Length 6159;
Best Local Similarity 80.8%; Pred. No. 4.1e-46;
RESULT 930
ID AAD32327 standard; DNA; 15765 BP.
DE Human NFKB1B gene, alternative version.
PN WO200212497-A2.
PD 14-FEB-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 21.9%; Score 198.2; DB 6; Length 15765;
Best Local Similarity 79.2%; Pred. No. 5.8e-46;
RESULT 931
ID AAD32179 standard; DNA; 15765 BP.
DE Human NFKB1B gene.
PN WO200212497-A2.
PD 14-FEB-2002.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 21.9%; Score 198.2; DB 6; Length 15765;
Best Local Similarity 79.2%; Pred. No. 5.8e-46;
RESULT 932
ID AAK74096 standard; DNA; 21777 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28908.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.9%; Score 198.2; DB 4; Length 21777;
Best Local Similarity 80.5%; Pred. No. 6.6e-46;
RESULT 933
ID AAS17764 standard; DNA; 24843 BP.
DE Human genomic DNA for CRYBL.
PN WO200185998-A1.
PD 15-NOV-2001.
PA (GENA-) GENAISSANCE PHARM INC.
Query Match 21.9%; Score 198.2; DB 6; Length 24843;
Best Local Similarity 81.7%; Pred. No. 6.9e-46;
RESULT 934
ID ADR67086 standard; DNA; 29328 BP.
DE Human cancer associated gene genomic sequence SEQ ID NO:132.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.2; DB 13; Length 29328;
Best Local Similarity 77.4%; Pred. No. 7.4e-46;
RESULT 935
ID AAL04340 standard; DNA; 32194 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 7028.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 21.9%; Score 198.2; DB 4; Length 32194;
Best Local Similarity 82.9%; Pred. No. 7.7e-46;
RESULT 936
ID ADS19371 standard; DNA; 37940 BP.
DE Human PIP5K type II beta related DNA #1.
PN US2003232777-A1.
PD 18-DEC-2003.
PA (MARC-) MARCUSSON B G.
PA (DOBI/) DOBIE K W.
PA (FREI/) FREIER S M.
Query Match 21.9%; Score 198.2; DB 13; Length 37940;
Best Local Similarity 75.9%; Pred. No. 8.2e-46;
RESULT 937
ID ADJ26093 standard; DNA; 38000 BP.
DE Human PIP5K1-beta genomic DNA SeqID 11.
PN US2003232775-A1.
PD 18-DEC-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.9%; Score 198.2; DB 12; Length 38000;
Best Local Similarity 75.9%; Pred. No. 8.2e-46;
RESULT 938
ID ACN45050 standard; DNA; 41966 BP.
DE Human genomic sequence hCG39344.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.9%; Score 198.2; DB 11; Length 41966;
Best Local Similarity 80.5%; Pred. No. 8.5e-46;
RESULT 939
ID ADB16927 standard; DNA; 49806 BP.
DE Human DYX1C1 DNA, chromosomal gene region nucleotides 50001-100000.
PN WO2003068814-A1.
PD 21-AUG-2003.
PA (LICN) LICENTIA LTD.
Query Match 21.9%; Score 198.2; DB 9; Length 49806;
Best Local Similarity 82.7%; Pred. No. 9.1e-46;
RESULT 940
ID ABD32754 standard; DNA; 62124 BP.
DE Human cancer-associated genomic DNA HD16-028.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.9%; Score 198.2; DB 13; Length 62124;
Best Local Similarity 82.9%; Pred. No. 9.9e-46;
RESULT 941
ID ADO25290 standard; DNA; 80928 BP.
DE Human protein kinase C iota/lambda genomic sequence.
PN WO2004041212-A2.
PD 21-MAY-2004.
PA (SACK/) SACKTOR T C.
PA (CRAR/) CRARY J F.
PA (HERN/) HERNANDEZ A I.
PA (MIRR/) MIRRA S.
PA (SHAO/) SHAO C.
Query Match 21.9%; Score 198.2; DB 12; Length 80928;
Best Local Similarity 79.4%; Pred. No. 1.1e-45;
RESULT 942
ID AAP84800 standard; DNA; 110000 BP.
DE Nucleotide sequence of the human SPG4 gene.
PN FR2798138-A1.
PD 09-MAR-2001.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 21.9%; Score 198.2; DB 5; Length 110000;
Best Local Similarity 80.5%; Pred. No. 1.2e-45;
RESULT 943
Query Match 21.9%; Score 198.2; DB 6; Length 110000;
Best Local Similarity 82.9%; Pred. No. 1.2e-45;
RESULT 944
ID AC013448 standard; DNA; 115756 BP.
DE Human DNA encoding a p53 modifier. SEQ ID 68.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.

Query Match 21.9%; Score 198.2; DB 8; Length 115756;
 Best Local Similarity 85.6%; Pred. No. 1.3e-45;
 RESULT 945
 ID ADJ79962 standard; DNA; 123526 BP.
 DE Human genome-associated oncogene-3 related DNA, SEQ ID NO 11.
 PN WO2003008549-A2.
 PD 30-JAN-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.9%; Score 198.2; DB 10; Length 123526;
 Best Local Similarity 81.9%; Pred. No. 1.3e-45;
 RESULT 946
 ID AAV57903 standard; DNA; 237326 BP.
 DE Hereditary haemochromatosis subregion from an HH affected individual.
 PN WO9814466-A1.
 PD 09-APR-1998.
 PA (PROG-) PROCENTOR INC.
 Query Match 21.9%; Score 198.2; DB 2; Length 237326;
 Best Local Similarity 82.9%; Pred. No. 1.7e-45;
 RESULT 947
 ID ADQ59422 standard; DNA; 246940 BP.
 DE Human cancer-associated (CA) gene sequence SEQ ID NO:58.
 PN WO2004058289-A1.
 PD 15-UTL-2004.
 PA (SAGE-) SAGES DISCOVERY INC.
 Query Match 21.9%; Score 198.2; DB 12; Length 246940;
 Best Local Similarity 78.9%; Pred. No. 1.7e-45;
 RESULT 948
 ID ADC87010 standard; DNA; 349999 BP.
 DE Human GPCR gene SEQ ID NO:11463.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 Query Match 21.9%; Score 198.2; DB 10; Length 349999;
 Best Local Similarity 75.5%; Pred. No. 1.9e-45;
 RESULT 949
 ID ADQ24208 standard; DNA; 1911 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7028.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.8%; Score 198; DB 12; Length 1911;
 Best Local Similarity 78.0%; Pred. No. 3e-46;
 RESULT 950
 ID ADM01910 standard; cDNA; 2460 BP.
 DE Human cDNA of the invention SEQ ID NO:595.
 PN EP1347046-A1.
 PD 24-SEP-2003.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Query Match 21.8%; Score 198; DB 11; Length 2460;
 Best Local Similarity 81.6%; Pred. No. 3.3e-46;
 RESULT 951
 ID AAK68971 standard; DNA; 7770 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23783.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 7770;
 Best Local Similarity 83.6%; Pred. No. 5.1e-46;
 RESULT 952
 ID AAK76477 standard; DNA; 9409 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:31289.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 9409;
 Best Local Similarity 81.2%; Pred. No. 5.5e-46;
 RESULT 953
 ID AAD34213 standard; DNA; 9432 BP.
 DE Human cytochrome P450 2D6 (CYP2D6) gene.
 PN WO200218638-A2.
 PD 07-MAR-2002.
 PA (GEMI-) GEMINI GENOMICS PLC.

Query Match 21.8%; Score 198; DB 6; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 954
 ID ACA61301 standard; DNA; 9432 BP.
 DE Human cytochrome P450 gene CYP2D6, wild-type.
 PN EP1281755-A2.
 PD 05-FEB-2003.
 PA (PFIZ-) PFIZER PROD INC.
 Query Match 21.8%; Score 198; DB 10; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 955
 ID ADF83400 standard; DNA; 9432 BP.
 DE Human CYP2D6 gene (wild-type).
 PN WO2003100091-A1.
 PD 04-DEC-2003.
 PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.
 Query Match 21.8%; Score 198; DB 12; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 956
 ID ADJ78563 standard; DNA; 9432 BP.
 DE Human cytochrome P450 isoenzyme 2D6 genomic gene sequence SeqID1.
 PN WO2004009760-A2.
 PD 29-JAN-2004.
 PA (BIOV-) BIOVENTURES INC.
 Query Match 21.8%; Score 198; DB 12; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 957
 ID ADM28891 standard; DNA; 9432 BP.
 DE Human wild-type CYP2D6 gene sequence.
 PN US2004072235-A1.
 PD 15-APR-2004.
 PA (DAMS/) DAMSON E P.
 Query Match 21.8%; Score 198; DB 12; Length 9432;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 958
 ID ACA61302 standard; DNA; 9433 BP.
 DE Human cytochrome P450 gene CYP2D6, variant sequence.
 PN EP1281755-A2.
 PD 05-FEB-2003.
 PA (PFIZ-) PFIZER PROD INC.
 Query Match 21.8%; Score 198; DB 10; Length 9433;
 Best Local Similarity 81.4%; Pred. No. 5.5e-46;
 RESULT 959
 ID AAL06376 standard; DNA; 11557 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9064.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;
 RESULT 960
 ID AAL06375 standard; DNA; 11557 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9063.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 4; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;
 RESULT 961
 ID AAS32244 standard; DNA; 11557 BP.
 DE Human DNA repair and processing genomic DNA #30.
 PN WO200155204-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 5; Length 11557;
 Best Local Similarity 82.6%; Pred. No. 5.9e-46;
 RESULT 962
 ID AAS32243 standard; DNA; 11557 BP.
 DE Human DNA repair and processing genomic DNA #29.
 PN WO200155204-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 198; DB 5; Length 11557;

Best Local Similarity 82.6%; Pred. No. 5.9e-46;
ID ABA07814 standard; DNA; 32191 BP.
DE Novel human DNA repair protein, genomic sequence #30.
PN US2002086353-A1.
PD 04-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.8%; Score 198; DB 6; Length 11557;
Best Local Similarity 82.6%; Pred. No. 5.9e-46;
RESULT 964
ID ABA07814 standard; DNA; 11557 BP.
DE Novel human DNA repair protein, genomic sequence #29.
PN US2002086353-A1.
PD 04-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.8%; Score 198; DB 6; Length 11557;
Best Local Similarity 82.6%; Pred. No. 5.9e-46;
RESULT 965
ID ABA079132 standard; DNA; 14379 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:33944.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 14379;
Best Local Similarity 83.8%; Pred. No. 6.4e-46;
RESULT 966
ID ABA079132 standard; DNA; 19472 BP.
DE Human genomic DNA encoding partial novel secreted protein, Seq ID 1698.
PN WO200155322-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 19472;
Best Local Similarity 75.1%; Pred. No. 7.2e-46;
RESULT 967
ID ABA074073 standard; DNA; 19472 BP.
DE Human novel polynucleotide #901.
PN US2002132753-A1.
PD 19-SEP-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.8%; Score 198; DB 8; Length 19472;
Best Local Similarity 75.1%; Pred. No. 7.2e-46;
RESULT 968
ID ABA03615 standard; DNA; 32134 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6303.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 32134;
Best Local Similarity 82.4%; Pred. No. 8.7e-46;
RESULT 969
ID ABA07813 standard; DNA; 32134 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 608.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 32134;
Best Local Similarity 82.4%; Pred. No. 8.7e-46;
RESULT 970
ID ABA03616 standard; DNA; 32191 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6304.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 32191;
Best Local Similarity 82.4%; Pred. No. 8.8e-46;
RESULT 971
ID ABA07814 standard; DNA; 32191 BP.
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 609.
PN WO200155325-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 32191;
Best Local Similarity 82.4%; Pred. No. 8.8e-46;
RESULT 972
ID ABA0618 standard; DNA; 32220 BP.
DE Human nervous system related polynucleotide SEQ ID NO 12949.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 5; Length 32220;
Best Local Similarity 80.1%; Pred. No. 8.8e-46;
RESULT 973
ID ABA061804 standard; DNA; 40645 BP.
DE Genomic DNA encoding novel human GABA transporter related protein.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY B M.
Query Match 21.8%; Score 198; DB 8; Length 40645;
Best Local Similarity 76.7%; Pred. No. 9.6e-46;
RESULT 974
ID ABA049717 standard; DNA; 40645 BP.
DE Genomic DNA encoding human transporter protein.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY B M.
Query Match 21.8%; Score 198; DB 8; Length 40645;
Best Local Similarity 76.7%; Pred. No. 9.6e-46;
RESULT 975
ID ABA071437 standard; DNA; 52845 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:26249.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 198; DB 4; Length 52845;
Best Local Similarity 83.5%; Pred. No. 1.1e-45;
RESULT 976
ID ABA04918 standard; DNA; 55114 BP.
DE Human genomic sequence hCG20493.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 198; DB 11; Length 55114;
Best Local Similarity 82.4%; Pred. No. 1.1e-45;
RESULT 977
ID ABA02684 standard; DNA; 59817 BP.
DE Human DUSP10 carcinoma associated gene, SEQ ID NO:1202.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 198; DB 9; Length 59817;
Best Local Similarity 82.6%; Pred. No. 1.1e-45;
RESULT 978
ID ABA072422 standard; DNA; 59817 BP.
DE Human DUSP10 gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 198; DB 10; Length 59817;
Best Local Similarity 82.6%; Pred. No. 1.1e-45;
RESULT 979
ID ABA05932 standard; DNA; 59817 BP.
DE Human DUSP10 gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 198; DB 10; Length 59817;
Best Local Similarity 82.6%; Pred. No. 1.1e-45;
RESULT 980
ID ABA02934 standard; DNA; 70000 BP.
DE Human phospholipase A2 (PLA2), group VI (Ca2+-independent) gene.

PN US6410325-B1.
 PD 25-JUN-2002.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.8%; Score 198; DB 6; Length 70000;
 Best Local Similarity 80.1%; Pred. No. 1.2e-45;
 RESULT 981
 ID ACN44938 standard; DNA; 73771 BP.
 DE Human genomic sequence hCG37394.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.8%; Score 198; DB 11; Length 73771;
 Best Local Similarity 82.8%; Pred. No. 1.2e-45;
 RESULT 982
 ID AAL57572 standard; cDNA; 107818 BP.
 DE Human phosphomannomutase 1 cDNA.
 PN WO2003059148-A2.
 PD 24-JUL-2003.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.8%; Score 198; DB 9; Length 107818;
 Best Local Similarity 80.8%; Pred. No. 1.4e-45;
 RESULT 983
 Query Match 21.8%; Score 198; DB 10; Length 110000;
 Best Local Similarity 75.1%; Pred. No. 1.4e-45;
 RESULT 984
 Query Match 21.8%; Score 198; DB 10; Length 110000;
 Best Local Similarity 75.1%; Pred. No. 1.4e-45;
 RESULT 985
 ID ADQ19183 standard; DNA; 110665 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2002.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.8%; Score 198; DB 12; Length 110665;
 Best Local Similarity 76.0%; Pred. No. 1.4e-45;
 RESULT 986
 ID ADQ17641 standard; DNA; 114771 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 458.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Query Match 21.8%; Score 198; DB 12; Length 114771;
 Best Local Similarity 78.8%; Pred. No. 1.4e-45;
 RESULT 987
 ID ADQ97319 standard; DNA; 117829 BP.
 DE Human cancer associated sequence HD08-031, SEQ ID 296.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.8%; Score 198; DB 12; Length 117829;
 Best Local Similarity 76.0%; Pred. No. 1.4e-45;
 RESULT 988
 ID ADH63063 standard; DNA; 132762 BP.
 DE Human fibroblast growth factor receptor 2 related sequence, SEQ ID 17.
 PN WO2003024987-A1.
 PD 27-MAR-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.8%; Score 198; DB 10; Length 132762;
 Best Local Similarity 82.6%; Pred. No. 1.5e-45;
 RESULT 989
 ID AAK84797 standard; cDNA; 149671 BP.
 DE Human cDNA differentially expressed in granulocytic cells #1368.
 PN WO200228899-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.8%; Score 198; DB 6; Length 149671;
 Best Local Similarity 83.8%; Pred. No. 1.6e-45;
 RESULT 990
 ID ADB70361 standard; cDNA; 149671 BP.
 DE Moebln cDNA SEQ ID NO:53.
 PN WO2003021229-A2.
 PD 13-MAR-2003.

PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 21.8%; Score 198; DB 9; Length 149671;
 Best Local Similarity 83.8%; Pred. No. 1.6e-45;
 RESULT 991
 ID ADJ37140 standard; cDNA; 149671 BP.
 DE Human malignant pleural mesothelioma. (MPM) cDNA #23.
 PN US2003219760-A1.
 PD 27-NOV-2003.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 Query Match 21.8%; Score 198; DB 12; Length 149671;
 Best Local Similarity 83.8%; Pred. No. 1.6e-45;
 RESULT 992
 ID ADL13752 standard; DNA; 190000 BP.
 DE Osteoarthritis-associated polymorphic nucleotide #284.
 PN WO2003054166-A2.
 PD 03-JUL-2003.
 PA (INCY-) INCYTE GENOMICS INC.
 Query Match 21.8%; Score 198; DB 10; Length 190000;
 Best Local Similarity 81.2%; Pred. No. 1.7e-45;
 RESULT 993
 ID ADF14037 standard; DNA; 1167 BP.
 DE Human endometrial-specific DNA - SEQ ID 2.
 PN WO2003059927-A1.
 PD 24-JUL-2003.
 PA (DIAD-) DIADEXUS INC.
 Query Match 21.8%; Score 197.8; DB 10; Length 1167;
 Best Local Similarity 75.7%; Pred. No. 2.8e-46;
 RESULT 994
 ID AAC69633 standard; cDNA; 1295 BP.
 DE Human secreted protein gene 37 SEQ ID NO:47.
 PN WO200056882-A1.
 PD 28-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.8%; Score 197.8; DB 3; Length 1295;
 Best Local Similarity 77.5%; Pred. No. 2.9e-46;
 RESULT 995
 ID AAK35888 standard; cDNA; 3705 BP.
 DE cDNA sequence #279 encoding novel human secreted protein.
 PN WO200177289-A2.
 PD 18-OCT-2001.
 PA (GENY) GENETICS INST INC.
 Query Match 21.8%; Score 197.8; DB 6; Length 3705;
 Best Local Similarity 78.0%; Pred. No. 4.3e-46;
 RESULT 996
 ID AAI57935 standard; cDNA; 6610 BP.
 DE Human polynucleotide SEQ ID NO 138.
 PN WO200153112-A1.
 PD 26-JUL-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 6610;
 Best Local Similarity 82.1%; Pred. No. 5.4e-46;
 RESULT 997
 ID AAK51636 standard; cDNA; 7005 BP.
 DE Human polynucleotide SEQ ID NO 181.
 PN WO200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 21.8%; Score 197.8; DB 4; Length 7005;
 Best Local Similarity 82.1%; Pred. No. 5.6e-46;
 RESULT 998
 ID AAK58061 standard; DNA; 16707 BP.
 DE Genomic DNA for Human GABAB receptors.
 PN WO9921890-A1.
 PD 06-MAY-1999.
 PA (ASTR) ASTRA AB.
 Query Match 21.8%; Score 197.8; DB 2; Length 16707;
 Best Local Similarity 80.7%; Pred. No. 7.8e-46;
 RESULT 999
 ID AAI03177 standard; DNA; 21913 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 6065.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 21.8%; Score 197.8; DB 4; Length 21913;
Best Local Similarity 77.9%; Pred. No. 8.6e-46;
RESULT 1000
ID AAL03378 standard; DNA; 21913 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6066.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.8; DB 4; Length 21913;
Best Local Similarity 77.9%; Pred. No. 8.6e-46;
RESULT 1001
ID AAL03379 standard; DNA; 21913 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 6067.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.8; DB 4; Length 21913;
Best Local Similarity 77.9%; Pred. No. 8.6e-46;
RESULT 1002
ID AAK70624 standard; DNA; 24768 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 25436.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.8; DB 4; Length 24768;
Best Local Similarity 80.5%; Pred. No. 9e-46;
RESULT 1003
ID ADI81379 standard; DNA; 25001 BP.
DE Human P2X4 genomic DNA sequence.
PN US2004002152-A1.
PD 01-JAN-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.8%; Score 197.8; DB 12; Length 25001;
Best Local Similarity 76.9%; Pred. No. 9.1e-46;
RESULT 1004
ID ADH36221 standard; DNA; 28616 BP.
DE Human purinergic receptor P2X4 gene sequence.
PN WO2003101177-A2.
PD 11-DEC-2003.
PA (SEQU-) SEQUENOM INC.
Query Match 21.8%; Score 197.8; DB 12; Length 28616;
Best Local Similarity 76.9%; Pred. No. 9.6e-46;
RESULT 1005
ID AAS32492 standard; DNA; 32191 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID NO 446.
PN WO200155313-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.8; DB 4; Length 32191;
Best Local Similarity 77.5%; Pred. No. 1e-45;
RESULT 1006
ID ACN44490 standard; DNA; 32865 BP.
DE Human genomic sequence hCG25375.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 197.8; DB 11; Length 32865;
Best Local Similarity 78.5%; Pred. No. 1e-45;
RESULT 1007
ID AAK71918 standard; DNA; 42048 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 26730.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.8; DB 4; Length 42048;
Best Local Similarity 79.6%; Pred. No. 1.1e-45;
RESULT 1008
ID AAG44140 standard; DNA; 50000 BP.
DE Nucleotide sequence of a beta-tubulin antigen.
PN WO200050593-A1.
PD 31-AUG-2000.
PA (UYTE-) UNIV TENNESSEE RES CORP.
Query Match 21.8%; Score 197.8; DB 3; Length 50000;

Best Local Similarity 81.7%; Pred. No. 1.2e-45;
RESULT 1009
ID AAD30228 standard; DNA; 53522 BP.
DE Human PKD1 gene.
PN WO200206529-A2.
PD 24-JAN-2002.
PA (UYJO-) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
Query Match 21.8%; Score 197.8; DB 6; Length 53522;
Best Local Similarity 80.5%; Pred. No. 1.2e-45;
RESULT 1010
ID AAT94101 standard; DNA; 53526 BP.
DE Human PKD1 gene.
PN WO9744457-A1.
PD 27-NOV-1997.
PA (GENZ-) GENZYME CORP.
Query Match 21.8%; Score 197.8; DB 2; Length 53526;
Best Local Similarity 80.5%; Pred. No. 1.2e-45;
RESULT 1011
ID AAT18551 standard; DNA; 53577 BP.
DE Human polycystic kidney disease normal PKD1 gene.
PN WO9612033-A1.
PD 25-APR-1996.
PA (IGIG-) IG LAB INC.
Query Match 21.8%; Score 197.8; DB 2; Length 53577;
Best Local Similarity 80.5%; Pred. No. 1.2e-45;
RESULT 1012
ID AAT94108 standard; DNA; 53577 BP.
DE Human PKD1 locus between chromosomal markers ATP6 (ATP6C) and D16S84.
PN WO9744457-A1.
PD 27-NOV-1997.
PA (GENZ-) GENZYME CORP.
Query Match 21.8%; Score 197.8; DB 2; Length 53577;
Best Local Similarity 80.5%; Pred. No. 1.2e-45;
RESULT 1013
ID AAK83212 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 38024.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.8; DB 4; Length 68356;
Best Local Similarity 80.5%; Pred. No. 1.3e-45;
RESULT 1014
ID AAK67283 standard; DNA; 68356 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 22095.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.8; DB 4; Length 68356;
Best Local Similarity 80.5%; Pred. No. 1.3e-45;
RESULT 1015
ID ACN44710 standard; DNA; 70242 BP.
DE Human genomic sequence hCG1784894.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 197.8; DB 11; Length 70242;
Best Local Similarity 80.7%; Pred. No. 1.3e-45;
RESULT 1016
ID ADR53001 standard; DNA; 96256 BP.
DE Drug therapy altered expressed gene #352.
PN WO2004072265-A2.
PD 26-AUG-2004.
PA (AMHP-) WYETH.
PA (BURC-) BURCZYNSKI M.
PA (TWIN-) TWINE N.
PA (DORN-) DORNER A J.
PA (TREP-) TREPCICHO W L.
Query Match 21.8%; Score 197.8; DB 13; Length 96256;
Best Local Similarity 80.7%; Pred. No. 1.5e-45;
RESULT 1017
ID ABR12169 standard; DNA; 98690 BP.
DE Human DNA representing the Tachykinin Receptor 1, TACR1, gene.

PN WO200216399-A2.
PD 28-FEB-2002.
PA (GENA-) GENAISANCE PHARM INC.
Query Match 21.8%; Score 197.8; DB 6; Length 98690;
Best Local Similarity 84.5%; Pred. No. 1.5e-45;
RESULT 1018
ID ABT44365 standard; DNA; 113000 BP.
DE Partial genomic sequence of human oestrogen receptor beta DNA.
PN WO2003050133-A1.
PD 19-JUN-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.8%; Score 197.8; DB 9; Length 113000;
Best Local Similarity 84.5%; Pred. No. 1.6e-45;
RESULT 1019
ID ADE43581 standard; DNA; 128034 BP.
DE Human IDE genomic sequence, SEQ ID 186.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO-) GEN HOSPITAL CORP.
Query Match 21.8%; Score 197.8; DB 10; Length 128034;
Best Local Similarity 79.6%; Pred. No. 1.7e-45;
RESULT 1020
ID ADH54059 standard; DNA; 128034 BP.
DE Human IDE gene DNA sequence SeqID186.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO-) GEN HOSPITAL CORP.
Query Match 21.8%; Score 197.8; DB 12; Length 128034;
Best Local Similarity 79.6%; Pred. No. 1.7e-45;
RESULT 1021
ID ACN44074 standard; DNA; 128668 BP.
DE Human genomic sequence hCG40471.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGES DISCOVERY.
Query Match 21.8%; Score 197.8; DB 11; Length 128668;
Best Local Similarity 80.7%; Pred. No. 1.7e-45;
RESULT 1022
ID ACA64895 standard; DNA; 134292 BP.
DE Human GABBR1 DNA corresponding to AL031983.
PN DE10127572-A1.
PD 05-DEC-2002.
PA (PATH-) PATHOARRAY GMBH.
Query Match 21.8%; Score 197.8; DB 8; Length 134292;
Best Local Similarity 80.7%; Pred. No. 1.7e-45;
RESULT 1023
ID ABK83562 standard; cDNA; 139904 BP.
DE Human cDNA differentially expressed in granulocytic cells #133.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.8%; Score 197.8; DB 6; Length 139904;
Best Local Similarity 81.7%; Pred. No. 1.8e-45;
RESULT 1024
ID AAZ86967 standard; DNA; 162450 BP.
DE Retinoblastoma binding protein-7 genomic DNA sequence.
PN WO20000607-A1.
PD 06-JAN-2000.
PA (GIST-) GIST.
Query Match 21.8%; Score 197.8; DB 3; Length 162450;
Best Local Similarity 80.7%; Pred. No. 1.9e-45;
RESULT 1025
ID ADE43315 standard; DNA; 202100 BP.
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.
PN WO2003054143-A2.
PD 03-JUL-2003.
PA (NEUR-) NEUROGENETICS INC.
PA (GEO-) GEN HOSPITAL CORP.
Query Match 21.8%; Score 197.8; DB 10; Length 202100;
Best Local Similarity 79.6%; Pred. No. 2e-45;
RESULT 1026
ID ADH54357 standard; DNA; 202100 BP.

DE Human IDE/ KNSL1 gene DNA sequence SeqID484.
PN US2003224380-A1.
PD 04-DEC-2003.
PA (GEO-) GEN HOSPITAL CORP.
Query Match 21.8%; Score 197.8; DB 12; Length 202100;
Best Local Similarity 79.6%; Pred. No. 2e-45;
RESULT 1027
ID ADB6352 standard; DNA; 300000 BP.
DE Human PTPN11 genomic DNA sequence SEQ ID NO:33.
PN WO2003029422-A2.
PD 10-APR-2003.
PA (MOUN-) MOUNT SINAI SCHOOL MEDICINE.
Query Match 21.8%; Score 197.8; DB 10; Length 300000;
Best Local Similarity 82.3%; Pred. No. 2.4e-45;
RESULT 1028
ID ADO14076 standard; DNA; 300001 BP.
DE Human protein tyrosine phosphatase 11 gene sequence SEQ ID NO:33.
PN WO2004041216-A2.
PD 21-MAY-2004.
PA (MOUN-) MOUNT SINAI SCHOOL MEDICINE.
PA (UNIV-) UNIVERSITÄTSKLINIKUM FREIBURG.
Query Match 21.8%; Score 197.8; DB 12; Length 300001;
Best Local Similarity 82.3%; Pred. No. 2.4e-45;
RESULT 1029
ID AAS43104 standard; DNA; 325791 BP.
DE Human Oestrogen receptor beta gene.
PN WO200162793-A2.
PD 30-AUG-2001.
PA (PEKE-) PE CORP NY.
Query Match 21.8%; Score 197.8; DB 4; Length 325791;
Best Local Similarity 84.5%; Pred. No. 2.4e-45;
RESULT 1030
ID ABX61844 standard; DNA; 601 BP.
DE Novel human transporter protein related polynucleotide #40.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 21.8%; Score 197.6; DB 8; Length 601;
Best Local Similarity 76.4%; Pred. No. 2.5e-46;
RESULT 1031
ID ABX61842 standard; DNA; 601 BP.
DE Novel human transporter protein related polynucleotide #38.
PN US2002142381-A1.
PD 03-OCT-2002.
PA (GONG/) GONG F.
PA (KERC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Query Match 21.8%; Score 197.6; DB 8; Length 601;
Best Local Similarity 76.4%; Pred. No. 2.5e-46;
RESULT 1032
ID ADF30333 standard; cDNA; 993 BP.
DE Human cancer suppressing protein p12616-encoding cDNA, SEQ:25 and 27.
PN CN1368508-A.
PD 11-SEP-2002.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 21.8%; Score 197.6; DB 10; Length 993;
Best Local Similarity 77.0%; Pred. No. 3e-46;
RESULT 1033
ID AAH14398 standard; cDNA; 2182 BP.
DE Human cDNA sequence SEQ ID NO:11832.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 21.8%; Score 197.6; DB 4; Length 2182;
Best Local Similarity 84.3%; Pred. No. 4e-46;
RESULT 1034
ID ABK35751 standard; cDNA; 2702 BP.
DE cDNA sequence #142 encoding novel human secreted protein.
PN WO200177289-A2.

PD 18-OCT-2001.
PA (GENV) GENETICS INST INC.
Query Match 21.8%; Score 197.6; DB 6; Length 2702;
Best Local Similarity 84.3%; Pred. No. 4.4e-46;
RESULT 1035
ID ABV75593 standard; DNA; 3509 BP.
DE Novel human gene #6.
PN WO200277257-A1.
PD 03-OCT-2002.
PA (HISE-) HISEQ INC.
Query Match 21.8%; Score 197.6; DB 10; Length 3509;
Best Local Similarity 84.3%; Pred. No. 4.9e-46;
RESULT 1036
ID AAK3051 standard; DNA; 5331 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37865.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 5331;
Best Local Similarity 80.5%; Pred. No. 5.7e-46;
RESULT 1037
ID AAK3051 standard; DNA; 7022 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:37863.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 7022;
Best Local Similarity 80.5%; Pred. No. 6.3e-46;
RESULT 1038
ID AAK3820 standard; DNA; 11840 BP.
DE Humane immune/haematopoietic antigen genomic sequence SEQ ID NO:38632.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 11840;
Best Local Similarity 76.4%; Pred. No. 7.8e-46;
RESULT 1039
ID AAS28506 standard; DNA; 23626 BP.
DE Genomic sequence #346 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1040
ID ABA2148 standard; DNA; 23626 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13811.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 5; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1041
ID AAS2997 standard; DNA; 23626 BP.
DE Human lung antigen genomic DNA #67.
PN WO200155303-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 5; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1042
ID AD33334 standard; DNA; 23626 BP.
DE Human novel lung related polypeptide DNA SEQ ID NO 261.
PN US2003054368-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 10; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1043
ID AD641702 standard; DNA; 23626 BP.
DE Human respiratory system associated genomic DNA seq id 940.
PN US2003215893-A1.
PD 20-NOV-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 10; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1044
ID AD197476 standard; DNA; 23626 BP.
DE Human respiratory system associated polypeptide-related DNA seqID940.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 11; Length 23626;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1045
ID AAS28507 standard; DNA; 23632 BP.
DE Genomic sequence #347 encoding for novel human respiratory antigen.
PN WO200155448-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1046
ID ABA21481 standard; DNA; 23632 BP.
DE Human nervous system related polynucleotide SEQ ID NO 13812.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 5; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1047
ID AAS29998 standard; DNA; 23632 BP.
DE Human lung antigen genomic DNA #68.
PN WO200155303-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 5; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1048
ID ADB33335 standard; DNA; 23632 BP.
DE Human novel lung related polypeptide DNA SEQ ID NO 262.
PN US2003054368-A1.
PD 20-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 10; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1049
ID AD641703 standard; DNA; 23632 BP.
DE Human respiratory system associated genomic DNA seq id 941.
PN US2003215893-A1.
PD 20-NOV-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 10; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1050
ID AD197477 standard; DNA; 23632 BP.
DE Human respiratory system associated polypeptide-related DNA seqID941.
PN US2003077704-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 11; Length 23632;
Best Local Similarity 77.1%; Pred. No. 1e-45;
RESULT 1051
ID ADL27170 standard; DNA; 29040 BP.
DE Human genomic sequence for LFNG.
PN US2003216558-A1.
PD 20-NOV-2003.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 21.8%; Score 197.6; DB 11; Length 29040;
Best Local Similarity 84.3%; Pred. No. 1.1e-45;
RESULT 1052
ID ADA03092 standard; DNA; 29322 BP.
DE Human LFNG carcinoma associated gene, SEQ ID NO:1610.
PN WO2003057146-A2.
PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 197.6; DB 9; Length 29322;
Best Local Similarity 84.3%; Pred. No. 1.1e-45;
RESULT 1053
ID ADA66376 standard; DNA; 29322 BP.
DE Human LTRNG gene genomic DNA sequence.
PN WO2003053224-A2.
PD 03-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 197.6; DB 9; Length 29322;
Best Local Similarity 84.3%; Pred. No. 1.1e-45;
RESULT 1054
ID ADB72830 standard; DNA; 29322 BP.
DE Human LTRNG gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 197.6; DB 10; Length 29322;
Best Local Similarity 84.3%; Pred. No. 1.1e-45;
RESULT 1055
ID AAK6677 standard; DNA; 34269 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23489.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 34269;
Best Local Similarity 74.4%; Pred. No. 1.2e-45;
RESULT 1056
ID AAK85168 standard; DNA; 34269 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39980.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.8%; Score 197.6; DB 4; Length 34269;
Best Local Similarity 74.4%; Pred. No. 1.2e-45;
RESULT 1057
ID ADS86040 standard; DNA; 37797 BP.
DE Tumour treatment-related human gene sequence SegID76.
PN WO2004034995-A2.
PD 29-APR-2004.
PA (UYPT-) UNIV PITTSBURGH.
Query Match 21.8%; Score 197.6; DB 13; Length 37797;
Best Local Similarity 80.3%; Pred. No. 1.2e-45;
RESULT 1058
ID ACN44534 standard; DNA; 39768 BP.
DE Human genomic sequence hCG38101.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 197.6; DB 11; Length 39768;
Best Local Similarity 78.1%; Pred. No. 1.2e-45;
RESULT 1059
ID ABD33318 standard; DNA; 52987 BP.
DE Human cancer-associated (CA) gene HD07-057.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.8%; Score 197.6; DB 13; Length 52987;
Best Local Similarity 77.1%; Pred. No. 1.4e-45;
RESULT 1060
ID ACC45150 standard; DNA; 96649 BP.
DE Human NAC nucleotide sequence SEQ ID NO:10.
PN WO2003024988-A1.
PD 27-MAR-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.8%; Score 197.6; DB 8; Length 96649;
Best Local Similarity 80.3%; Pred. No. 1.7e-45;
RESULT 1061
ID ACB36634 standard; cDNA; 463 BP.
DE Human endothelial cell cDNA #4767.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
Query Match 21.8%; Score 197.6; DB 12; Length 110000;
Best Local Similarity 73.6%; Pred. No. 1.8e-45;
RESULT 1062
ID ACH36634 standard; cDNA; 463 BP.
DE Human endothelial cell cDNA #4767.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
Query Match 21.8%; Score 197.6; DB 12; Length 110000;
Best Local Similarity 73.6%; Pred. No. 1.8e-45;

RESULT 1063
ID ACA64961 standard; DNA; 152141 BP.
DE Human BCR DNA corresponding to U07000.
PN DE10127572-A1.
PD 05-DEC-2002.
PA (PATH-) PATHOARRAY GMBH.
Query Match 21.8%; Score 197.6; DB 8; Length 152141;
Best Local Similarity 84.0%; Pred. No. 2.1e-45;
RESULT 1064
ID AAK83571 standard; cDNA; 175737 BP.
DE Human cDNA differentially expressed in granulocytic cells #142.
PN WO200228999-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.8%; Score 197.6; DB 6; Length 175737;
Best Local Similarity 76.6%; Pred. No. 2.2e-45;
RESULT 1065
ID ADL13596 standard; DNA; 175737 BP.
DE Osteoarthritis-associated polymorphic nucleotide #128.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.8%; Score 197.6; DB 10; Length 175737;
Best Local Similarity 76.6%; Pred. No. 2.2e-45;
RESULT 1066
ID ADQ18934 standard; DNA; 175737 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1753.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.8%; Score 197.6; DB 12; Length 175737;
Best Local Similarity 76.6%; Pred. No. 2.2e-45;
RESULT 1067
ID ACN44010 standard; DNA; 198522 BP.
DE Human genomic sequence hCG1643869.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.8%; Score 197.6; DB 11; Length 198522;
Best Local Similarity 78.7%; Pred. No. 2.3e-45;
RESULT 1068
ID ABS56564 standard; DNA; 260209 BP.
DE Human SUF2 genomic DNA sequence.
PN WO200259327-A2.
PD 01-AUG-2002.
PA (REGC) UNIV CALIFORNIA.
Query Match 21.8%; Score 197.6; DB 6; Length 260209;
Best Local Similarity 86.3%; Pred. No. 2.6e-45;
RESULT 1069
ID ADN16204 standard; DNA; 260209 BP.
DE Human sulfatase SUF1 gene.
PN WO2004031365-A2.
PD 15-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 21.8%; Score 197.6; DB 12; Length 260209;
Best Local Similarity 86.9%; Pred. No. 2.6e-45;
RESULT 1070
ID ABK89296 standard; DNA; 326014 BP.
DE Human gene for novel serine/threonine kinase.
PN WO2004031365-A2.
PD 15-APR-2004.
PA (REGC) UNIV CALIFORNIA.
Query Match 21.8%; Score 197.6; DB 6; Length 326014;
Best Local Similarity 80.3%; Pred. No. 2.8e-45;
RESULT 1071
ID ADQ94981 standard; DNA; 326014 BP.
DE Human kinase genomic DNA.
Query Match 21.8%; Score 197.6; DB 12; Length 326014;
Best Local Similarity 80.3%; Pred. No. 2.8e-45;
RESULT 1072
ID ACH36634 standard; cDNA; 463 BP.
DE Human endothelial cell cDNA #4767.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
Query Match 21.8%; Score 197.6; DB 12; Length 326014;
Best Local Similarity 80.3%; Pred. No. 2.8e-45;

PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 9; Length 463;
RESULT 1073
ID ADB83200 standard; cDNA; 588 BP.
DE Human cDNA sequence useful for the treatment of cancer (SeqID 1413).
PN WO2003050236-A2.
PD 19-JUN-2003.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 9; Length 588;
RESULT 1074
ID AAH98452 standard; cDNA; 874 BP.
DE Human EST-derived coding sequence SEQ ID NO: 309.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 4; Length 874;
RESULT 1075
ID ADG10849 standard; cDNA; 1599 BP.
DE Human STAT6-activating protein-encoding cDNA, SEQ ID NO:439.
PN WO200296943-A1.
PD 05-DEC-2002.
PA (ASAH) ASAH KASEI KOGYO KK.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 10; Length 1599;
RESULT 1076
ID AAK75888 standard; DNA; 3891 BP.
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:30700.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 4; Length 3891;
RESULT 1077
ID AAK90709 standard; DNA; 5032 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 4285.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 4; Length 5032;
RESULT 1078
ID ABD33436 standard; DNA; 52710 BP.
DE Human cancer-associated (CA) gene HD07-082.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 13; Length 52710;
RESULT 1079
ID ABD33470 standard; DNA; 61765 BP.
DE Human cancer-associated (CA) gene HD07-090.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 13; Length 61765;
RESULT 1080
ID ACN44362 standard; DNA; 68255 BP.
DE Human genomic sequence hCG39597.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 11; Length 68255;
RESULT 1081
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 6; Length 110000;

Best Local Similarity 84.8%; Pred. No. 2.1e-45;
RESULT 1082
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 6; Length 110000;
RESULT 1083
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 8; Length 110000;
RESULT 1084
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 12; Length 110000;
RESULT 1085
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 12; Length 110000;
RESULT 1086
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 13; Length 110000;
RESULT 1087
ID ABL68122 standard; DNA; 174424 BP.
DE Ovary cancer related gene sequence SEQ ID NO:6459.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALLON PHARM.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 6; Length 174424;
RESULT 1088
ID ADQ19573 standard; DNA; 181343 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2392.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 21.8%; Score 197.4; DB 12; Length 181343;
RESULT 1089
ID AAT62346 standard; DNA; 282 BP.
DE Consensus Alu repeat sequence.
PN US5597694-A.
PD 28-JAN-1997.
PA (MAST) MASSACHUSETTS INST TECHNOLOGY.
Query Match
Best Local Similarity 21.7%; Score 197.2; DB 2; Length 282;
RESULT 1090
ID AAF22565 standard; cDNA; 537 BP.
DE Human breast cancer associated antigen nucleotide sequence SEQ ID NO:144.
PN WO200073801-A2.
PD 07-DEC-2000.
PA (LUDM-) LUDWIG INST CANCER RES.
Query Match
Best Local Similarity 21.7%; Score 197.2; DB 4; Length 537;
RESULT 1091
ID ABN61073 standard; cDNA; 662 BP.
DE Human cancer related polynucleotide SEQ ID NO 1040.
PN WO200214500-A2.
PD 21-FEB-2002.
PA (CHIR) CHIRON CORP.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 21.7%; Score 197.2; DB 6; Length 662;
RESULT 1092
ID ACC86725 standard; DNA; 751 BP.
DE Human VEGFR-1 nucleotide sequence SEQ ID NO:20.
PN WO2003022237-A2.
PD 20-MAR-2003.
PA (ISIS-) ISIS PHARM INC.
Query Match
Best Local Similarity 21.7%; Score 197.2; DB 8; Length 751;
RESULT 1093
ID AAH16580 standard; cDNA; 2092 BP.
DE Human cDNA sequence SEQ ID NO:15661.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match
Best Local Similarity 21.7%; Score 197.2; DB 4; Length 2092;

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RESULT 1094
ID ADF81697 standard; DNA; 4908 BP.
DE Leukemia-related DNA sequence #2253.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFB/) HAFERLACH T.
PA (SCHC/) SCHUCH C.
PA (KERN/) KERN W.
Query Match 21.7%; Score 197.2; DB 10; Length 4908;
Best Local Similarity 72.4%; Pred. No. 7.2e-46;
RESULT 1095
ID ADF81698 standard; DNA; 4908 BP.
DE Leukemia-related DNA sequence #2254.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFB/) HAFERLACH T.
PA (SCHC/) SCHUCH C.
PA (KERN/) KERN W.
Query Match 21.7%; Score 197.2; DB 10; Length 4908;
Best Local Similarity 72.4%; Pred. No. 7.2e-46;
RESULT 1096
ID AAK73007 standard; DNA; 6658 BP.
DE Human immune/haematopoietic antigen genomic*sequence SEQ ID NO:27819.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 6658;
Best Local Similarity 83.3%; Pred. No. 8.1e-46;
RESULT 1097
ID AAL03021 standard; DNA; 6658 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 5709.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 6658;
Best Local Similarity 83.3%; Pred. No. 8.1e-46;
RESULT 1098
ID AAL06167 standard; DNA; 8577 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8855.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 8577;
Best Local Similarity 81.8%; Pred. No. 8.9e-46;
RESULT 1099
ID ABL98732 standard; DNA; 8577 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3384.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 8577;
Best Local Similarity 81.8%; Pred. No. 8.9e-46;
RESULT 1100
ID ABA17047 standard; DNA; 8577 BP.
DE Human nervous system related polynucleotide SEQ ID NO 9378.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 5; Length 8577;
Best Local Similarity 81.8%; Pred. No. 8.9e-46;
RESULT 1101
ID AAK8986 standard; DNA; 32224 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3562.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 32224;
Best Local Similarity 84.2%; Pred. No. 1.5e-45;
RESULT 1102
ID ABD33190 standard; DNA; 33478 BP.
DE Human cancer-associated (CA) gene HD07-028.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.7%; Score 197.2; DB 13; Length 33478;
Best Local Similarity 84.2%; Pred. No. 1.5e-45;
RESULT 1103
ID ABN96830 standard; DNA; 40433 BP.
DE Gene #3328 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.7%; Score 197.2; DB 6; Length 40433;
Best Local Similarity 80.5%; Pred. No. 1.6e-45;
RESULT 1104
ID ADA02528 standard; DNA; 57763 BP.
DE Human MYB carcinoma associated gene, SEQ ID NO:1046.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 197.2; DB 9; Length 57763;
Best Local Similarity 80.5%; Pred. No. 1.9e-45;
RESULT 1105
ID ADB72266 standard; DNA; 57763 BP.
DE Human MYB gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 197.2; DB 10; Length 57763;
Best Local Similarity 80.5%; Pred. No. 1.9e-45;
RESULT 1106
ID ADE95776 standard; DNA; 57763 BP.
DE Human MYB gene genomic DNA sequence.
PN WO2003039484-A2.
PD 15-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 197.2; DB 10; Length 57763;
Best Local Similarity 80.5%; Pred. No. 1.9e-45;
RESULT 1107
ID ADJ53477 standard; DNA; 70000 BP.
DE Human PPP3CB genomic DNA #3.
PN US2004023382-A1.
PD 05-FEB-2004.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.7%; Score 197.2; DB 12; Length 70000;
Best Local Similarity 85.8%; Pred. No. 2e-45;
RESULT 1108
ID AAK85590 standard; DNA; 75384 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40402.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 197.2; DB 4; Length 75384;
Best Local Similarity 80.3%; Pred. No. 2.1e-45;
RESULT 1109
ID ADJ33364 standard; DNA; 92139 BP.
DE 92kb gene fragment in human chromosome 17 at 17q21.
PN WO200210455-A2.
PD 07-FEB-2002.
PA (CEL-) CELLTECH R & D INC.
Query Match 21.7%; Score 197.2; DB 6; Length 92139;
Best Local Similarity 80.5%; Pred. No. 2.2e-45;
RESULT 1110
ID AAD53324 standard; DNA; 567571 BP.
DE Human chromosome 3 q-arm breakpoint region.
PN WO200290541-A1.
PD 14-NOV-2002.
PA (MURD-) MURDOCH CHILDRENS RES INST.
PA (DELA/) DELATYCKI M.
Query Match 21.7%; Score 197.2; DB 8; Length 110000;
Best Local Similarity 84.5%; Pred. No. 2.4e-45;
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RESULT 1111
Query Match      21.7%; Score 197.2; DB 11; Length 110000;
Best Local Similarity 78.9%; Pred. No. 2.4e-45;
RESULT 1112
Query Match      21.7%; Score 197.2; DB 11; Length 110000;
Best Local Similarity 78.9%; Pred. No. 2.4e-45;
RESULT 1113
Query Match      21.7%; Score 197.2; DB 11; Length 110000;
Best Local Similarity 74.0%; Pred. No. 2.4e-45;
RESULT 1114
ID ADH76849 standard; DNA; 122557 BP.
DE Melanin-concentrating hormone receptor 1 locus clone.
PN WO2003104489-A2.
PD 18-DEC-2003.
PA (UYRH-) UNIV PHILIPPS MARBURG.
Query Match      21.7%; Score 197.2; DB 12; Length 122557;
Best Local Similarity 78.6%; Pred. No. 2.5e-45;
RESULT 1115
ID ADO80254 standard; cDNA; 127145 BP.
DE Hernandez-Pudlak syndrome associated cDNA.
PN WO2004063709-A2.
PD 29-JUL-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match      21.7%; Score 197.2; DB 13; Length 127145;
Best Local Similarity 74.6%; Pred. No. 2.5e-45;
RESULT 1116
ID ADR11613 standard; DNA; 130320 BP.
DE Human sclerostin gene region.
PN WO2003087763-A2.
PD 23-OCT-2003.
PA (CELL-) CELLTECH R & D INC.
PA (UYRO-) UNIV ROTTERDAM ERASMUS.
Query Match      21.7%; Score 197.2; DB 10; Length 130320;
Best Local Similarity 80.5%; Pred. No. 2.5e-45;
RESULT 1117
ID ADQ97183 standard; DNA; 138627 BP.
DE Human cancer associated sequence HD08-011, SEQ ID 159.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match      21.7%; Score 197.2; DB 12; Length 138627;
Best Local Similarity 84.5%; Pred. No. 2.6e-45;
RESULT 1118
ID AAI95194 standard; cDNA; 717 BP.
DE Human neuroblastoma expressed polynucleotide SEQ ID NO 1269.
PN WO200166719-A1.
PD 13-SEP-2001.
PA (CHIB-) CHIBA PREFECTURE.
PA (HISM) HISAMITSU PHARM CO LTD.
Query Match      21.7%; Score 197; DB 4; Length 717;
Best Local Similarity 75.1%; Pred. No. 3.9e-46;
RESULT 1119
ID AAS32730 standard; DNA; 1515 BP.
DE Human genomic DNA for novel endocrine antigen, SEQ ID No 684.
PN WO200155319-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      21.7%; Score 197; DB 4; Length 1515;
Best Local Similarity 82.4%; Pred. No. 5.2e-46;
RESULT 1120
ID ABL55355 standard; cDNA; 2408 BP.
DE Human protein synthesis initiation factor 10.12-encoding cDNA.
PN CN1331221-A.
PD 16-JAN-2002.
PA (BOBE-) BOBE GENE DEV CO LTD SHANGHAI.
Query Match      21.7%; Score 197; DB 6; Length 2408;
Best Local Similarity 80.0%; Pred. No. 6.3e-46;
RESULT 1121
ID ACC50229 standard; cDNA; 2969 BP.
DE Breast cancer associated cDNA sequence SEQ ID NO:301.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match      21.7%; Score 197; DB 8; Length 2969;
Best Local Similarity 82.5%; Pred. No. 6.8e-46;
RESULT 1122
ID ADR07810 standard; cDNA; 3779 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1316.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match      21.7%; Score 197; DB 13; Length 3779;
Best Local Similarity 83.7%; Pred. No. 7.4e-46;
RESULT 1123
ID ADR08449 standard; cDNA; 3834 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1955.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match      21.7%; Score 197; DB 13; Length 3834;
Best Local Similarity 78.9%; Pred. No. 7.5e-46;
RESULT 1124
ID ADR07292 standard; cDNA; 3868 BP.
DE Full length human cDNA useful for treating neurological disease Seq 798.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match      21.7%; Score 197; DB 13; Length 3868;
Best Local Similarity 78.9%; Pred. No. 7.5e-46;
RESULT 1125
ID AAK85025 standard; DNA; 5919 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39837.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      21.7%; Score 197; DB 4; Length 5919;
Best Local Similarity 79.2%; Pred. No. 8.8e-46;
RESULT 1126
ID AAZ59353 standard; DNA; 8396 BP.
DE Human SRP2 (phenol sulphotransferase 2) gene.
PN WO9964630-A1.
PD 16-DEC-1999.
PA (AXYS-) AXYS PHARM INC.
Query Match      21.7%; Score 197; DB 3; Length 8396;
Best Local Similarity 74.2%; Pred. No. 1e-45;
RESULT 1127
ID AAK89550 standard; DNA; 13246 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3126.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      21.7%; Score 197; DB 4; Length 13246;
Best Local Similarity 82.5%; Pred. No. 1.2e-45;
RESULT 1128
ID AAK89551 standard; DNA; 13247 BP.
DE Human digestive system antigen genomic sequence SEQ ID NO: 3127.
PN WO200155314-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match      21.7%; Score 197; DB 4; Length 13247;
Best Local Similarity 82.5%; Pred. No. 1.2e-45;
RESULT 1129
ID ABD32570 standard; DNA; 22047 BP.
DE Human cancer-associated genomic DNA HD7-165.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match      21.7%; Score 197; DB 13; Length 22047;
Best Local Similarity 77.9%; Pred. No. 1.5e-45;
RESULT 1130
ID ABD33137 standard; DNA; 22056 BP.
DE Human cancer-associated (CA) gene HD07-016.
PN WO2004058146-A2.
PD 15-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match      21.7%; Score 197; DB 13; Length 22056;
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Best Local Similarity 77.9%; Pred. No. 1.5e-45;
 RESULT 1131
 ID AAK61639 standard; DNA; 28011 BP.
 DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:36451.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 28011;
 Best Local Similarity 82.4%; Pred. No. 1.6e-45;
 RESULT 1132
 ID ADC67584 standard; DNA; 28066 BP.
 DE Human GPCR gene SEQ ID NO:2037.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 DE (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 21.7%; Score 197; DB 10; Length 28066;
 Best Local Similarity 77.9%; Pred. No. 1.6e-45;
 RESULT 1133
 ID AAK90296 standard; DNA; 32199 BP.
 DE Human digestive system antigen genomic sequence SEQ ID NO: 3872.
 PN WO200155314-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1134
 ID AAI5673 standard; DNA; 32199 BP.
 DE Human colorectal cancer antigen coding sequence SEQ ID NO: 210.
 PN WO200155350-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 4; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1135
 ID ABS9850 standard; DNA; 32199 BP.
 DE Genomic DNA #54 encoding human colorectal cancer related protein.
 PN US2002119919-A1.
 PD 29-AUG-2002.
 PA (ROSE/) ROSEN C A.
 PA (RUBE/) RUBEN S M.
 PA (BAR/) BARASH S C.
 Query Match 21.7%; Score 197; DB 6; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1136
 ID ADB93003 standard; DNA; 32199 BP.
 DE Human colorectal cancer related polypeptide DNA #54.
 PN US2003054420-A1.
 PD 20-MAR-2003.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 197; DB 10; Length 32199;
 Best Local Similarity 74.2%; Pred. No. 1.7e-45;
 RESULT 1137
 ID ADQ5482 standard; DNA; 43709 BP.
 DE Human cancer-associated (CA) gene sequence SEQ ID NO:118.
 PN WO2004058288-A1.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 197; DB 12; Length 43709;
 Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1138
 ID ACN45130 standard; DNA; 61197 BP.
 DE Human genomic sequence hCG15017.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 61197;
 Best Local Similarity 77.3%; Pred. No. 2.2e-45;
 RESULT 1139
 ID ACN44082 standard; DNA; 71048 BP.
 DE Human genomic sequence hCG39199.
 PN WO2003073826-A2.
 PD 12-SEP-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 71048;
 Best Local Similarity 83.7%; Pred. No. 2.3e-45;
 RESULT 1140
 ID ACN44422 standard; DNA; 114931 BP.
 DE Human genomic sequence hCG27894.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 114931;
 Best Local Similarity 80.0%; Pred. No. 2.8e-45;
 RESULT 1141
 ID AAV52850 standard; DNA; 116792 BP.
 DE Human eyal gene contig 4405-9480.
 PN WO9832849-A2.
 PD 30-JUL-1998.
 PA (INSP-) INST PASTEUR.
 Query Match 21.7%; Score 197; DB 2; Length 116792;
 Best Local Similarity 80.0%; Pred. No. 2.8e-45;
 RESULT 1143
 ID ACN44574 standard; DNA; 116792 BP.
 DE Human genomic sequence hCG18576.
 PN WO2003073826-A2.
 PD 12-SEP-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 197; DB 11; Length 116792;
 Best Local Similarity 79.2%; Pred. No. 2.8e-45;
 RESULT 1144
 ID ADI29095 standard; DNA; 119501 BP.
 DE Human MARK3 genomic DNA.
 PN US2003232771-A1.
 PD 18-DEC-2003.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.7%; Score 197; DB 12; Length 119501;
 Best Local Similarity 79.8%; Pred. No. 2.8e-45;
 RESULT 1145
 ID ADH50806 standard; DNA; 119596 BP.
 DE Human G-protein coupled receptor gene.
 PN US2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 Query Match 21.7%; Score 197; DB 6; Length 119596;
 Best Local Similarity 77.3%; Pred. No. 2.8e-45;
 RESULT 1146
 ID ADE43582 standard; DNA; 128034 BP.
 DE Polymorphic human IDB genomic sequence, SEQ ID 187.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 Query Match 21.7%; Score 197; DB 10; Length 128034;
 Best Local Similarity 80.0%; Pred. No. 2.9e-45;
 RESULT 1147
 ID ADE43581 standard; DNA; 128034 BP.
 DE Human IDB genomic sequence, SEQ ID 186.
 PN WO2003054143-A2.
 PD 03-JUL-2003.
 PA (NEUR-) NEUROGENETICS INC.
 Query Match 21.7%; Score 197; DB 10; Length 128034;
 Best Local Similarity 80.0%; Pred. No. 2.9e-45;
 RESULT 1148
 ID ADH54059 standard; DNA; 128034 BP.
 DE Human IDB gene DNA sequence SeqID186.
 PN US2003224380-A1.
 PD 04-DEC-2003.
 PA (GEHO-) GEN HOSPITAL CORP.
 Query Match 21.7%; Score 197; DB 12; Length 128034;
 Best Local Similarity 80.0%; Pred. No. 2.9e-45;
 RESULT 1149
 ID ADH54060 standard; DNA; 128034 BP.
 DE Human IDB gene variant DNA sequence SeqID187.
 PN US2003224380-A1.

PD 04-DEC-2003.
PA (GENO) GEN HOSPITAL CORP.
Query Match 21.7%; Score 197; DB 12; Length 128034;
Best Local Similarity 80.0%; Pred. No. 2.9e-45;
RESULT 1150
ID ABRN5735 standard; DNA; 155074 BP.
DE Human genomic region containing the ltrp5 gene SEQ ID NO 6.
PN WO200254069-A1.
PD 11-JUL-2002.
PA (RESC) UNIV CALIFORNIA.
Query Match 21.7%; Score 197; DB 6; Length 155074;
Best Local Similarity 81.1%; Pred. No. 3.1e-45;
RESULT 1151
ID ADQ040461 standard; DNA; 166181 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3281.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.7%; Score 197; DB 12; Length 166181;
Best Local Similarity 82.5%; Pred. No. 3.2e-45;
RESULT 1152
ID ADQ18633 standard; DNA; 166181 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1452.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.7%; Score 197; DB 12; Length 166181;
Best Local Similarity 82.5%; Pred. No. 3.2e-45;
RESULT 1153
ID ACN43946 standard; DNA; 174448 BP.
DE Human genomic sequence hCG21793.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGES DISCOVERY.
Query Match 21.7%; Score 197; DB 11; Length 174448;
Best Local Similarity 78.9%; Pred. No. 3.3e-45;
RESULT 1154
ID AD133935 standard; DNA; 177866 BP.
DE Osteoarthritis-associated polymorphic nucleotide #467.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.7%; Score 197; DB 10; Length 177866;
Best Local Similarity 84.0%; Pred. No. 3.3e-45;
RESULT 1155
ID ACN44598 standard; DNA; 212231 BP.
DE Human genomic sequence hCG401221.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGES DISCOVERY.
Query Match 21.7%; Score 197; DB 11; Length 212231;
Best Local Similarity 77.1%; Pred. No. 3.5e-45;
RESULT 1156
ID ACN44194 standard; DNA; 275449 BP.
DE Human genomic sequence hCG23995.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGES DISCOVERY.
Query Match 21.7%; Score 197; DB 11; Length 275449;
Best Local Similarity 80.0%; Pred. No. 3.9e-45;
RESULT 1157
ID AD862528 standard; cDNA; 2308 BP.
DE Human cDNA encoding clone HNDPC20082790.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 21.7%; Score 196.8; DB 10; Length 2308;
Best Local Similarity 78.5%; Pred. No. 7e-46;
RESULT 1158
ID ADQ66839 standard; cDNA; 2320 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3714.
PN WO2004060270-A2.

PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.8; DB 12; Length 2320;
Best Local Similarity 80.5%; Pred. No. 7e-46;
RESULT 1159
ID ADQ83620 standard; cDNA; 2320 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #434.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.8; DB 13; Length 2320;
Best Local Similarity 80.5%; Pred. No. 7e-46;
RESULT 1160
ID ADQ84294 standard; cDNA; 2320 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1108.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.8; DB 13; Length 2320;
Best Local Similarity 80.5%; Pred. No. 7e-46;
RESULT 1161
ID ADQ84044 standard; cDNA; 2320 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #858.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.8; DB 13; Length 2320;
Best Local Similarity 80.5%; Pred. No. 7e-46;
RESULT 1162
ID ACN40563 standard; cDNA; 2320 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA326655, SEQ ID NO:5419.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.8; DB 13; Length 2320;
Best Local Similarity 80.5%; Pred. No. 7e-46;
RESULT 1163
ID ADM02495 standard; cDNA; 2404 BP.
DE Human cDNA of the invention SEQ ID NO:1180.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.7%; Score 196.8; DB 11; Length 2404;
Best Local Similarity 78.5%; Pred. No. 7.1e-46;
RESULT 1164
ID ABO83600 standard; cDNA; 2631 BP.
DE Human fumarate reductase/succinic dehydrogenase 9.13 cDNA SEQ ID NO:1.
PN CN1345948-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 21.7%; Score 196.8; DB 6; Length 2631;
Best Local Similarity 84.7%; Pred. No. 7.4e-46;
RESULT 1165
ID AAK65744 standard; DNA; 5079 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21556.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMA GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 5079;
Best Local Similarity 79.5%; Pred. No. 9.5e-46;
RESULT 1166
ID ADQ24919 standard; DNA; 6833 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7739.
PN WO2004048938-A2.
PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.7%; Score 196.8; DB 12; Length 6833;
Best Local Similarity 84.7%; Pred. No. 1.1e-45;
RESULT 1167
ID ADQ24145 standard; DNA; 6833 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6965.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.7%; Score 196.8; DB 12; Length 6833;
Best Local Similarity 84.7%; Pred. No. 1.1e-45;
RESULT 1168
ID AAI62666 standard; DNA; 7444 BP.
DE Human breast or ovarian antigen genomic DNA SEQ ID NO: 316.
PN WO200155324-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 7444;
Best Local Similarity 83.4%; Pred. No. 1.1e-45;
RESULT 1169
ID AAL06760 standard; DNA; 7444 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9448.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 7444;
Best Local Similarity 83.4%; Pred. No. 1.1e-45;
RESULT 1170
ID AAL06118 standard; DNA; 7444 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 8806.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 7444;
Best Local Similarity 83.4%; Pred. No. 1.1e-45;
RESULT 1171
ID ABL96683 standard; DNA; 7444 BP.
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3335.
PN WO200155317-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 7444;
Best Local Similarity 83.4%; Pred. No. 1.1e-45;
RESULT 1172
ID ABA15667 standard; DNA; 7444 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8198.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 5; Length 7444;
Best Local Similarity 83.4%; Pred. No. 1.1e-45;
RESULT 1173
ID AAK66749 standard; DNA; 9324 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21561.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9324;
Best Local Similarity 79.5%; Pred. No. 1.2e-45;
RESULT 1174
ID AAS28695 standard; DNA; 9765 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID NO 257.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1175
ID AAS28886 standard; DNA; 9755 BP.
DE Human immunoglobulin encoding genomic DNA SEQ ID NO 248.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1176
ID ABA15616 standard; DNA; 15187 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7947.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1177
ID ABA06849 standard; DNA; 9765 BP.
DE Human genomic DNA SEQ ID NO: 935.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1178
ID ABA064139 standard; DNA; 9765 BP.
DE Human polynucleotide SEQ ID NO 888.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBS/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.7%; Score 196.8; DB 6; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1179
ID ABA06118 standard; DNA; 9765 BP.
DE Human polynucleotide SEQ ID NO 935.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBS/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 21.7%; Score 196.8; DB 6; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1180
ID ADB31736 standard; DNA; 9765 BP.
DE Human novel protein DNA SEQ ID NO 257.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 10; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1181
ID ADB31727 standard; DNA; 9765 BP.
DE Human novel protein DNA SEQ ID NO 248.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 10; Length 9765;
Best Local Similarity 78.0%; Pred. No. 1.2e-45;
RESULT 1182
ID AAS42100 standard; DNA; 12595 BP.
DE Genomic sequence #416 encoding novel human enzyme polypeptide.
PN WO200155301-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 4; Length 12595;
Best Local Similarity 80.5%; Pred. No. 1.4e-45;
RESULT 1183
ID ABA15617 standard; DNA; 15186 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7948.
PN WO2001559063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.8; DB 5; Length 15186;
Best Local Similarity 82.0%; Pred. No. 1.5e-45;
RESULT 1184
ID ABA15616 standard; DNA; 15187 BP.
DE Human nervous system related polynucleotide SEQ ID NO 7947.

PN WO200159063-A2.
 PD 16-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 5; Length 15187;
 DE Best Local Similarity 82.0%; Pred. No. 1.5e-45;
 RESULT 1185
 ID AAK6680 standard; DNA; 17357 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41492.
 PN WO20015182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 4; Length 17357;
 DE Best Local Similarity 83.2%; Pred. No. 1.5e-45;
 RESULT 1186
 ID AAK6681 standard; DNA; 17363 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41493.
 PN WO20015182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 4; Length 17363;
 DE Best Local Similarity 83.2%; Pred. No. 1.5e-45;
 RESULT 1187
 ID ADC6168 standard; DNA; 21704 BP.
 DE Human GPCR gene SEQ ID NO:621.
 PN EP1270724-A2.
 PD 02-JAN-2003.
 PA (MAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 DE (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
 Query Match 21.7%; Score 196.8; DB 10; Length 21704;
 DE Best Local Similarity 79.5%; Pred. No. 1.7e-45;
 RESULT 1188
 ID ADQ97776 standard; DNA; 25694 BP.
 DE Human cancer associated sequence HD10-045, SEQ ID 753.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 12; Length 25694;
 DE Best Local Similarity 78.5%; Pred. No. 1.8e-45;
 RESULT 1189
 ID ABS52813 standard; DNA; 27847 BP.
 DE Genomic DNA encoding human secreted protein #1.
 PN WO200264626-A2.
 PD 22-AUG-2002.
 PA (PEKE-) PE CORP NY.
 Query Match 21.7%; Score 196.8; DB 6; Length 27847;
 DE Best Local Similarity 81.8%; Pred. No. 1.8e-45;
 RESULT 1190
 ID ADQ97189 standard; DNA; 29360 BP.
 DE Human cancer associated sequence HD08-012, SEQ ID 165.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 12; Length 29360;
 DE Best Local Similarity 80.7%; Pred. No. 1.9e-45;
 RESULT 1191
 ID AAJ37292 standard; DNA; 32192 BP.
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 3657.
 PN WO200155367-A1.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 4; Length 32192;
 DE Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1192
 ID AAL07103 standard; DNA; 32192 BP.
 DE Human reproductive system related antigen DNA SEQ ID NO: 9791.
 PN WO200155320-A2.
 PD 02-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 4; Length 32192;
 DE Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1193
 ID ABX60280 standard; cDNA; 32192 BP.
 DE cDNA encoding novel human musculoskeletal system antigen #2624.

PN US2002147140-A1.
 PD 10-OCT-2002.
 PA (ROSE/) ROSEN C A.
 DE (RUBE/) RUBEN S M.
 PA (BARA/) BARASH S C.
 Query Match 21.7%; Score 196.8; DB 8; Length 32192;
 DE Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1194
 ID ADJ1030 standard; DNA; 32192 BP.
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3657.
 PN US2004009488-A1.
 PD 15-JAN-2004.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 12; Length 32192;
 DE Best Local Similarity 79.5%; Pred. No. 1.9e-45;
 RESULT 1195
 ID ABL64428 standard; DNA; 35641 BP.
 DE Stomach cancer related gene sequence SEQ ID NO:2765.
 PN WO200194629-A2.
 PD 13-DEC-2001.
 PA (AVAL-) AVALON PHARM.
 Query Match 21.7%; Score 196.8; DB 6; Length 35641;
 DE Best Local Similarity 82.0%; Pred. No. 2e-45;
 RESULT 1196
 ID ABN95727 standard; DNA; 35641 BP.
 DE Gene #2325 used to diagnose liver cancer.
 PN WO200228103-A2.
 PD 11-APR-2002.
 PA (GENE-) GENE LOGIC INC.
 Query Match 21.7%; Score 196.8; DB 6; Length 35641;
 DE Best Local Similarity 82.0%; Pred. No. 2e-45;
 RESULT 1197
 ID AAK72372 standard; DNA; 37925 BP.
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27184.
 PN WO200157182-A2.
 PD 09-AUG-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 21.7%; Score 196.8; DB 12; Length 37925;
 DE Best Local Similarity 79.5%; Pred. No. 2.1e-45;
 RESULT 1198
 ID ADJ12847 standard; DNA; 37925 BP.
 DE DNA fragment of a BAC clone that encodes a human secreted protein Seq701.
 PN US2004010132-A1.
 PD 15-JAN-2004.
 PA (ROSE/) ROSEN C A.
 DE (BREM/) BREWER L A.
 PA (DUAN/) DUAN R D.
 PA (RUBE/) RUBEN S M.
 PA (FLOR/) FLORENCE K A.
 PA (GRE/) GREENE J M.
 PA (YOUN/) YOUNG P E.
 PA (FERR/) FERRIE A M.
 PA (YUG/) YU G.
 PA (FLOR/) FLORENCE C.
 PA (EBNE/) EBNER R.
 PA (OLSE/) OLSEN H.
 Query Match 21.7%; Score 196.8; DB 12; Length 37925;
 DE Best Local Similarity 79.5%; Pred. No. 2.1e-45;
 RESULT 1199
 ID ABK65018 standard; DNA; 43545 BP.
 DE Human cadherin-like asymmetry protein-2 (CLASP-2) genomic DNA.
 PN WO200231117-A2.
 PD 18-APR-2002.
 PA (ARBO-) ARBOR VITA CORP.
 PA (GARW/) GARMAN J D.
 PA (CAND/) CANDIA A F.
 Query Match 21.7%; Score 196.8; DB 6; Length 43545;
 DE Best Local Similarity 76.9%; Pred. No. 2.2e-45;
 RESULT 1200
 ID ADA02960 standard; DNA; 44325 BP.
 DE Human DAD1 carcinoma associated gene, SEQ ID NO:1478.
 PN WO2003057146-A2.
 PD 17-JUL-2003.

PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.8; DB 9; Length 44325;
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1201
 ID ADB72698 standard; DNA; 44325 BP.
 DE Human DAD1 gene.
 PN WO2003008563-A2.
 PD 30-JAN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.8; DB 10; Length 44325;
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1202
 ID ADC85440 standard; DNA; 44325 BP.
 DE Human Dad1 genomic sequence.
 PN WO2003045230-A2.
 PD 05-JUN-2003.
 PA (SAGR-) SAGRES DISCOVERY.
 Query Match 21.7%; Score 196.8; DB 10; Length 44325;
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1203
 ID ADM74555 standard; DNA; 44325 BP.
 DE Human carcinoma associated (CA) nucleic acid #112.
 PN US2004072154-A1.
 PD 15-APR-2004.
 PA (MORR/) MORRIS D W.
 PA (ENGEL/) ENGELHARD E K.
 Query Match 21.7%; Score 196.8; DB 12; Length 44325;
 Best Local Similarity 82.0%; Pred. No. 2.2e-45;
 RESULT 1204
 ID ABD32574 standard; DNA; 45944 BP.
 DE Human cancer-associated genomic DNA HD7-204.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 13; Length 45944;
 Best Local Similarity 81.8%; Pred. No. 2.2e-45;
 RESULT 1205
 ID AAD42934 standard; DNA; 70000 BP.
 DE Human phospholipase A2 (PLA2), group VI (Ca2+-independent) gene.
 PN US641032-B1.
 PD 25-JUN-2002.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.7%; Score 196.8; DB 6; Length 70000;
 Best Local Similarity 79.5%; Pred. No. 2.6e-45;
 RESULT 1206
 Query Match 21.7%; Score 196.8; DB 12; Length 87411;
 Best Local Similarity 79.1%; Pred. No. 2.8e-45;
 RESULT 1207
 ID ABD33432 standard; DNA; 106938 BP.
 DE Human cancer-associated (CA) gene HD07-081.
 PN WO2004058146-A2.
 PD 15-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 13; Length 106938;
 Best Local Similarity 81.8%; Pred. No. 3.1e-45;
 RESULT 1208
 ID ADR67034 standard; DNA; 106938 BP.
 DE Human cancer associated gene genomic sequence SEQ ID NO.80.
 PN WO2004074321-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 21.7%; Score 196.8; DB 13; Length 106938;
 Best Local Similarity 81.8%; Pred. No. 3.1e-45;
 RESULT 1209
 ID ADL17884 standard; cDNA; 158001 BP.
 DE Human phosphotyrosyl phosphatase activator, PTPA, gene.
 PN US2004023906-A1.
 PD 05-FEB-2004.
 PA (ISIS-) ISIS PHARM INC.
 Query Match 21.7%; Score 196.8; DB 12; Length 158001;
 Best Local Similarity 84.5%; Pred. No. 3.6e-45;
 RESULT 1210
 ID ACA64924 standard; DNA; 201239 BP.

DE Human PLZF DNA corresponding to AF060568.
 PN DE10127572-A1.
 PD 05-DEC-2002.
 PA (PATR-) PATHOARRAY GMBH.
 Query Match 21.7%; Score 196.8; DB 8; Length 201239;
 Best Local Similarity 80.7%; Pred. No. 3.9e-45;
 RESULT 1211
 ID AAA69691 standard; cDNA; 461 BP.
 DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO.1.
 PN WO2000036107-A2.
 PD 22-JUN-2000.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 3; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1212
 ID AAA69693 standard; cDNA; 461 BP.
 DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO.3.
 PN WO2000036107-A2.
 PD 22-JUN-2000.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 3; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1213
 ID ABR72587 standard; DNA; 461 BP.
 DE Ovarian carcinoma antigen polynucleotide #3.
 PN WO200206317-A2.
 PD 24-JAN-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 6; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1214
 ID ABR72585 standard; DNA; 461 BP.
 DE Ovarian carcinoma antigen polynucleotide #1.
 PN WO200206317-A2.
 PD 24-JAN-2002.
 PA (CORI-) CORIXA CORP.
 Query Match 21.7%; Score 196.6; DB 6; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1215
 ID ADA08752 standard; DNA; 461 BP.
 DE Human ovarian carcinoma antigen polynucleotide #3.
 PN US2003091580-A1.
 PD 15-MAY-2003.
 PA (MITC/) MITCHAM J L.
 PA (KING/) KING G E.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 PA (RETT/) RETTER M W.
 PA (FANG/) FANGER G R.
 PA (REED/) REED S G.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (HILL/) HILL P.
 PA (ALBO/) ALBONE E.
 Query Match 21.7%; Score 196.6; DB 9; Length 461;
 Best Local Similarity 72.4%; Pred. No. 4.3e-46;
 RESULT 1216
 ID ADA08750 standard; DNA; 461 BP.
 DE Human ovarian carcinoma antigen polynucleotide #1.
 PN US2003091580-A1.
 PD 15-MAY-2003.
 PA (MITC/) MITCHAM J L.
 PA (KING/) KING G E.
 PA (ALGA/) ALGATE P A.
 PA (FLIN/) FLING S P.
 PA (RETT/) RETTER M W.
 PA (FANG/) FANGER G R.
 PA (REED/) REED S G.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (HILL/) HILL P.
 PA (ALBO/) ALBONE E.
 Query Match 21.7%; Score 196.6; DB 9; Length 461;


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Best Local Similarity 72.4%; Pred. No. 4.3e-46;
RESULT 1217
ID ADP08499 standard; cDNA; 461 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 3.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 21.7%; Score 196.6; DB 10; Length 461;
Best Local Similarity 72.4%; Pred. No. 4.3e-46;
RESULT 1218
ID ADP08497 standard; cDNA; 461 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 1.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Query Match 21.7%; Score 196.6; DB 10; Length 461;
Best Local Similarity 72.4%; Pred. No. 4.3e-46;
RESULT 1219
ID ADG46247 standard; cDNA; 461 BP.
DE Human ovarian carcinoma polynucleotide #3.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Query Match 21.7%; Score 196.6; DB 10; Length 461;
Best Local Similarity 72.4%; Pred. No. 4.3e-46;
RESULT 1220
ID ADG46245 standard; cDNA; 461 BP.
DE Human ovarian carcinoma polynucleotide #1.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Query Match 21.7%; Score 196.6; DB 10; Length 461;
Best Local Similarity 72.4%; Pred. No. 4.3e-46;
RESULT 1221
ID AAH15355 standard; cDNA; 1652 BP.
DE Human cDNA sequence SEQ ID NO:13531.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELT-) HELIX RES INST.
Query Match 21.7%; Score 196.6; DB 4; Length 1652;
Best Local Similarity 80.2%; Pred. No. 7.1e-46;
RESULT 1222
ID AAS21268 standard; cDNA; 3719 BP.
DE Human cDNA sequence encoding for PRO4799 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 4; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1223
ID ACA03627 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 8; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1224
ID ABX69165 standard; cDNA; 3719 BP.
DE DNA encoding novel secreted and transmembrane protein PRO4799.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 8; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1225
ID ACD1819 standard; cDNA; 3719 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #25.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 8; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1226
ID ACA04048 standard; cDNA; 3719 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 49.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 8; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1227
ID ADA45568 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003022328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1228
ID ADA75999 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1229
ID ADA18649 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1230
ID ADA61272 standard; cDNA; 3719 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1231
ID ADB19057 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1232
ID ADB27598 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1233
ID ADA86077 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1234
ID ADB15641 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
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Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1235
ID ADA47427 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1236
ID ADA67222 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1237
ID ADB30229 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1238
ID ADA65525 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1239
ID ADA96737 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1240
ID ADA79041 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1241
ID ADA87180 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1242
ID ADB16382 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1243
ID ADA91474 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1253
ID ADA79041 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;

RESULT 1244
ID ADB14537 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1245
ID ADB18498 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1246
ID ADA93713 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1247
ID ADB19609 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1248
ID ADB12921 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1249
ID ACD98448 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1250
ID ADA74175 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1251
ID ADB24408 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1252
ID ADA81932 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1253
ID ADA79041 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;

ID ADA74895 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1254
ID ADA84973 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1255
ID ADA84421 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1256
ID ADB29677 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1257
ID ADA80205 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1258
ID ADA75447 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1259
ID ADA46672 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1260
ID ADB24968 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1261
ID ADA93144 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1262
ID ADB26494 standard; cDNA; 3719 BP.

DE cDNA encoding human PRO polypeptide #25.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1263
ID ADB30781 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1264
ID ADA60709 standard; cDNA; 3719 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1265
ID ADB23856 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide SEQ ID NO 49.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1266
ID ADA96185 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1267
ID ADA80757 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1268
ID ADA95633 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1269
ID ADB25942 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1270
ID ADB21427 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 9; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1271
ID ADA77206 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.

PN US2003068797-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1272
 ID ADB17946 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003077710-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1273
 ID ADA86629 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082709-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1274
 ID ADA87732 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082700-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1275
 ID ADA46120 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003054516-A1.
 PD 20-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1276
 ID ADB28150 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003082699-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1277
 ID ADB28702 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003082706-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1278
 ID ADA76654 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003059909-A1.
 PD 27-MAR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1279
 ID ADA88284 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003073213-A1.
 PD 17-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1280
 ID ADA97289 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003082686-A1.

PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1281
 ID ADB27046 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003022239-A1.
 PD 30-JAN-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1282
 ID ADB21979 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087344-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1283
 ID ADA66670 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003068793-A1.
 PD 10-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1284
 ID ADB22531 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003077711-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1285
 ID ADB23304 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide SEQ ID NO 49.
 PN US2003077712-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1286
 ID ADA92026 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082712-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1287
 ID ADB15089 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003087352-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1288
 ID ADB38341 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003082766-A1.
 PD 01-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1289
 ID ADB37789 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087347-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 9; Length 3719;

Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1290			
ID	ADB6661 standard; cDNA; 3719 BP.		
DE	Novel human secreted and transmembrane protein PRO4799 cDNA.		
PN	US2003082689-A1.		
PD	01-MAY-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 9;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1291			
ID	ADB89341 standard; cDNA; 3719 BP.		
DE	Human PRO polynucleotide #25.		
PN	US2003082698-A1.		
PD	01-MAY-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1292			
ID	ADB90073 standard; cDNA; 3719 BP.		
DE	Human PRO polynucleotide #25.		
PN	US2003082762-A1.		
PD	01-MAY-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1293			
ID	ADB319174 standard; cDNA; 3719 BP.		
DE	Novel human secreted and transmembrane protein PRO4799 cDNA.		
PN	US2003082694-A1.		
PD	01-MAY-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1294			
ID	ADB46797 standard; cDNA; 3719 BP.		
DE	Novel human secreted and transmembrane protein PRO4799 cDNA.		
PN	US2003082687-A1.		
PD	01-MAY-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1295			
ID	ADB86404 standard; cDNA; 3719 BP.		
DE	Human PRO polynucleotide #25.		
PN	US2003082697-A1.		
PD	01-MAY-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1296			
ID	ADB77009 standard; cDNA; 3719 BP.		
DE	Novel human secreted and transmembrane protein PRO4799 cDNA.		
PN	US2003082696-A1.		
PD	01-MAY-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1297			
ID	ADB34166 standard; cDNA; 3719 BP.		
DE	Human PRO polynucleotide SEQ ID NO 49.		
PN	US2003077717-A1.		
PD	24-APR-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1298			
ID	ADB35270 standard; cDNA; 3719 BP.		
DE	Human PRO polynucleotide SEQ ID NO 49.		
PN	US2003077719-A1.		
PD	24-APR-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1299			
ID	ADB35270 standard; cDNA; 3719 BP.		
DE	Human PRO polynucleotide SEQ ID NO 49.		
PN	US2003077719-A1.		
PD	24-APR-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1300			
ID	ADB35270 standard; cDNA; 3719 BP.		
DE	Human PRO polynucleotide SEQ ID NO 49.		
PN	US2003077719-A1.		
PD	24-APR-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1301			
ID	ADB35270 standard; cDNA; 3719 BP.		
DE	Human PRO polynucleotide SEQ ID NO 49.		
PN	US2003077719-A1.		
PD	24-APR-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1302			
ID	ADB35270 standard; cDNA; 3719 BP.		
DE	Human PRO polynucleotide SEQ ID NO 49.		
PN	US2003077719-A1.		
PD	24-APR-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1303			
ID	ADB35270 standard; cDNA; 3719 BP.		
DE	Human PRO polynucleotide SEQ ID NO 49.		
PN	US2003077719-A1.		
PD	24-APR-2003.		
PA	(GENTECH) GENENTECH INC.		
Query Match	21.7%;	Score 1	

[illegible]

ID ADCC60168 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087367-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1309
 ID ADC50643 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087361-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1310
 ID ADC65170 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003087362-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1311
 ID ADC54268 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087363-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1312
 ID ADC53329 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087364-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1313
 ID ADC58752 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087359-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1314
 ID ADC55630 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087360-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1315
 ID ADC58200 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein cDNA Seq ID49.
 PN US2003087346-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1316
 ID ADD02874 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003092104-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1317
 ID ADC89866 standard; cDNA; 3719 BP.

DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087346-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1318
 ID ADC69285 standard; cDNA; 3719 BP.
 DE cDNA encoding human PRO polypeptide #25.
 PN US2003194770-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1319
 ID ADC48174 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194773-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1320
 ID ADD09703 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194776-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1321
 ID ADD04278 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087354-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1322
 ID ADC80234 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003092103-A1.
 PD 15-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1323
 ID ADD10741 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194774-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1324
 ID ADC47622 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003194771-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1325
 ID ADC79682 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003087358-A1.
 PD 08-MAY-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 10; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1326
 ID ADD09151 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.

PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1327
ID ADD40864 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1328
ID ADD52003 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1329
ID ADD52743 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1330
ID ADD53295 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1331
ID ADD51451 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1332
ID ADD02250 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1333
ID ADD01684 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1334
ID ADD53866 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1335
ID ADD92183 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199030-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1336
ID ADD91079 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1337
ID ADE03693 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1338
ID ADE31990 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1339
ID ADE21922 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1340
ID ADD79146 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1341
ID ADE41682 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1342
ID ADE17499 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1343
ID ADD91631 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 10; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1344
ID ADE33094 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.

PA	(GETH) GENENTECH INC.	21.7%;	Score 196.6;	DB 10;	Length 3719;
Query Match					
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1345					
ID	AD833646 standard; cDNA; 3719 BP.				
DE	Novel human secreted and transmembrane protein PRO4799 CDNA.				
PN	US2003194791-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		21.7%;	Score 196.6;	DB 10;	Length 3719;
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1346					
ID	ADD96698 standard; cDNA; 3719 BP.				
DE	CDNA encoding human PRO polypeptide #25.				
PN	US2003207417-A1.				
PD	06-NOV-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		21.7%;	Score 196.6;	DB 10;	Length 3719;
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1347					
ID	ADD92735 standard; cDNA; 3719 BP.				
DE	Human PRO polynucleotide #25.				
PN	US2003194768-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		21.7%;	Score 196.6;	DB 10;	Length 3719;
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1348					
ID	AD819155 standard; cDNA; 3719 BP.				
DE	Human PRO polynucleotide #25.				
PN	US2003199025-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		21.7%;	Score 196.6;	DB 10;	Length 3719;
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1349					
ID	AD818603 standard; cDNA; 3719 BP.				
DE	Human PRO polynucleotide #25.				
PN	US2003199026-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		21.7%;	Score 196.6;	DB 10;	Length 3719;
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1350					
ID	AD842799 standard; cDNA; 3719 BP.				
DE	Human PRO polynucleotide #25.				
PN	US2003199033-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		21.7%;	Score 196.6;	DB 10;	Length 3719;
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1351					
ID	AD895588 standard; cDNA; 3719 BP.				
DE	Human PRO polynucleotide #25.				
PN	US2003199059-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		21.7%;	Score 196.6;	DB 10;	Length 3719;
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1352					
ID	AD822474 standard; cDNA; 3719 BP.				
DE	CDNA encoding human PRO polypeptide #25.				
PN	US2003199064-A1.				
PD	23-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		21.7%;	Score 196.6;	DB 10;	Length 3719;
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1353					
ID	ADD78592 standard; cDNA; 3719 BP.				
DE	CDNA encoding human PRO polypeptide #25.				
PN	US2003203429-A1.				
PD	30-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		21.7%;	Score 196.6;	DB 10;	Length 3719;
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1354					
ID	AD832542 standard; cDNA; 3719 BP.				
DE	Novel human secreted and transmembrane protein PRO4799 CDNA.				
PN	US2003194766-A1.				
PD	16-OCT-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		21.7%;	Score 196.6;	DB 10;	Length 3719;
Best Local Similarity		80.2%;	Pred. No. 9.6e-46;		
RESULT 1355					
ID	AD842234 standard; cDNA; 3719 BP.				
DE	Human PRO polynucleotide #25.				
PN	US2003199032-A1.				
PD	23-OCT-2003.				

Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1363			
ID ADP97175 standard; cDNA; 3719 BP.			
DE Human PRO polynucleotide #25.			
PN US2003207379-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.			
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1364			
ID ADG80239 standard; cDNA; 3719 BP.			
DE Human PRO polynucleotide #25.			
PN US2003207373-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.			
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1365			
ID ADG79687 standard; cDNA; 3719 BP.			
DE Human PRO polynucleotide #25.			
PN US2003207372-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.			
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1366			
ID ADH54979 standard; cDNA; 3719 BP.			
DE Novel human secreted and transmembrane protein PRO4799 cDNA.			
PN US2003207381-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.			
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1367			
ID ADH55531 standard; cDNA; 3719 BP.			
DE Novel human secreted and transmembrane protein PRO4799 cDNA.			
PN US2003207379-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.			
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1368			
ID ADI63750 standard; cDNA; 3719 BP.			
DE Novel human secreted and transmembrane protein PRO4799 cDNA.			
PN US2003207385-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.			
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1369			
ID ADI64699 standard; cDNA; 3719 BP.			
DE Novel human secreted and transmembrane protein PRO4799 cDNA.			
PN US2003207386-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.			
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1370			
ID ADI63198 standard; cDNA; 3719 BP.			
DE Novel human secreted and transmembrane protein PRO4799 cDNA.			
PN US2003207387-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.			
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
RESULT 1371			
ID ADH81612 standard; cDNA; 3719 BP.			
DE Novel human secreted and transmembrane protein PRO4799 cDNA.			
PN US2003207388-A1.			
PD 06-NOV-2003.			
PA (GETH) GENENTECH INC.			
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	
Query Match	21.7%;	Score 196.6; DB 10;	Length 3719;
Best Local Similarity	80.2%;	Pred. No. 9.6e-46;	

RESULT 1372	ID	ADH1060 standard; cDNA; 3719 BP.
	ID	Novel human secreted and transmembrane protein PRO4799 CDNA.
	PN	US2003207377-A1.
	PD	06-NOV-2003.
	PA	(GETH) GENENTECH INC.
	Query Match	21.7%; Score 196.6; DB 10; Length 3719;
	Best Local Similarity	80.2%; Pred. No. 9.6e-46;
	RESULT 1373	ID
	ID	ACD23877 standard; cDNA; 3719 BP.
	ID	Novel human secreted and transmembrane protein PRO4799 CDNA.
	PN	US2003032156-A1.
	PD	13-FEB-2003.
	PA	(GETH) GENENTECH INC.
	Query Match	21.7%; Score 196.6; DB 10; Length 3719;
	Best Local Similarity	80.2%; Pred. No. 9.6e-46;
	RESULT 1374	ID
	ID	ACA67018 standard; cDNA; 3719 BP.
	ID	cDNA encoding human PRO polypeptide #25.
	PN	US2003004311-A1.
	PD	02-JAN-2003.
	PA	(GETH) GENENTECH INC.
	Query Match	21.7%; Score 196.6; DB 10; Length 3719;
	Best Local Similarity	80.2%; Pred. No. 9.6e-46;
	RESULT 1375	ID
	ID	ADH82229 standard; cDNA; 3719 BP.
	ID	Novel human secreted and transmembrane protein PRO4799 CDNA.
	PN	US2003087355-A1.
	PD	08-MAY-2003.
	PA	(GETH) GENENTECH INC.
	Query Match	21.7%; Score 196.6; DB 11; Length 3719;
	Best Local Similarity	80.2%; Pred. No. 9.6e-46;
	RESULT 1376	ID
	ID	ADN15628 standard; cDNA; 3719 BP.
	ID	Novel human secreted and transmembrane protein PRO4799 CDNA.
	PN	US2003087353-A1.
	PD	08-MAY-2003.
	PA	(GETH) GENENTECH INC.
	Query Match	21.7%; Score 196.6; DB 11; Length 3719;
	Best Local Similarity	80.2%; Pred. No. 9.6e-46;
	RESULT 1377	ID
	ID	ADN16257 standard; cDNA; 3719 BP.
	ID	Novel human secreted and transmembrane protein PRO4799 CDNA.
	PN	US2003087385-A1.
	PD	08-MAY-2003.
	PA	(GETH) GENENTECH INC.
	Query Match	21.7%; Score 196.6; DB 11; Length 3719;
	Best Local Similarity	80.2%; Pred. No. 9.6e-46;
	RESULT 1378	ID
	ID	ADN15076 standard; cDNA; 3719 BP.
	ID	Novel human secreted and transmembrane protein PRO4799 CDNA.
	PN	US2003087356-A1.
	PD	08-MAY-2003.
	PA	(GETH) GENENTECH INC.
	Query Match	21.7%; Score 196.6; DB 11; Length 3719;
	Best Local Similarity	80.2%; Pred. No. 9.6e-46;
	RESULT 1379	ID
	ID	ADN14524 standard; cDNA; 3719 BP.
	ID	Novel human secreted and transmembrane protein PRO4799 CDNA.
	PN	US2003087357-A1.
	PD	08-MAY-2003.
	PA	(GETH) GENENTECH INC.
	Query Match	21.7%; Score 196.6; DB 11; Length 3719;
	Best Local Similarity	80.2%; Pred. No. 9.6e-46;
	RESULT 1380	ID
	ID	ADC80786 standard; cDNA; 3719 BP.
	ID	Novel human secreted and transmembrane protein PRO4799 CDNA.
	PN	US2003092115-A1.
	PD	15-MAY-2003.
	PA	(GETH) GENENTECH INC.
	Query Match	21.7%; Score 196.6; DB 11; Length 3719;
	Best Local Similarity	80.2%; Pred. No. 9.6e-46;
	RESULT 1381	ID
	ID	ADH80786 standard; cDNA; 3719 BP.
	ID	Novel human secreted and transmembrane protein PRO4799 CDNA.
	PN	US2003092115-A1.
	PD	15-MAY-2003.
	PA	(GETH) GENENTECH INC.
	Query Match	21.7%; Score 196.6; DB 12; Length 3719;
	Best Local Similarity	80.2%; Pred. No. 9.6e-46;
	RESULT 1381	ID

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ID ADJ76234 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US200310087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1382
ID ADJ87598 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1383
ID ADJ86002 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1384
ID ADJ75450 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1385
ID ADJ3026 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1386
ID ADJ23578 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1387
ID ADJ24221 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1388
ID ADJ87046 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1389
ID ADJ88912 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1390
ID ADJ18051 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1391
ID ADJ88360 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1392
ID ADJ94380 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1393
ID ADJ90791 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1394
ID ADJ94932 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1395
ID ADJ93042 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1396
ID ADJ34623 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1397
ID ADJ91938 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1398
ID ADJ90239 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1399
ID ADJ9186 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
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PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1400
ID ADG01965 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1401
ID ADG21751 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1402
ID ADG19821 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1403
ID ADP97727 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1404
ID ADG23944 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1405
ID ADP98298 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1406
ID ADG03129 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1407
ID ADP98850 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1408
ID ADG16435 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1409
ID ADG04894 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1410
ID ADG319161 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1411
ID ADG12998 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1412
ID ADG08055 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1413
ID ADG15225 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1414
ID ADP96623 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1415
ID ADG05808 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1416
ID ADG23392 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1417
ID ADG03681 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003207423-A1.
PD 06-NOV-2003.
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PA (GETH) GENENTECH INC. 21.7%; Score 196.6; DB 12; Length 3719;
 Query Match
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1418
 ID ADG54582 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207427-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1419
 ID ADG06879 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207350-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1420
 ID ADG07431 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207356-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1421
 ID ADG54926 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003194778-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1422
 ID ADG60590 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207390-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1423
 ID ADG61694 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207428-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1424
 ID ADG81895 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207358-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1425
 ID ADG57134 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207362-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1426
 ID ADG56582 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207364-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.

Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1427
 ID ADG55478 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207365-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1428
 ID ADG58238 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207368-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1429
 ID ADG70604 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207420-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1430
 ID ADG57686 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207363-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1431
 ID ADG53270 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207415-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1432
 ID ADG71156 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207421-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1433
 ID ADG81343 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003207805-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1434
 ID ADH30305 standard; cDNA; 3719 BP.
 DE Human PRO polynucleotide #25.
 PN US2003077723-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1435
 ID ADH11672 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207419-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Query Match 21.7%; Score 196.6; DB 12; Length 3719;
 Best Local Similarity 80.2%; Pred. No. 9.6e-46;
 RESULT 1436
 ID ADH11672 standard; cDNA; 3719 BP.
 DE Novel human secreted and transmembrane protein PRO4799 cDNA.
 PN US2003207419-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.

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RESULT 1436
ID ADG52094 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1437
ID ADG53822 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1438
ID ADG80791 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1439
ID ADG56030 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1440
ID ADH12296 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1441
ID ADG61142 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1442
ID ADH28229 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1443
ID ADG54374 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1444
ID ADG59414 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1445
ID ADI80838 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1446
ID ADG09581 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1447
ID ADI15052 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1448
ID ADG08929 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1449
ID ADI14384 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1450
ID ADI17979 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1451
ID ADJ63260 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1452
ID ADJ77155 standard; cDNA; 3719 BP.
DE Human PRO polynucleotide #25.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1453
ID ADJ65277 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1454
ID ADM27413 standard; cDNA; 3719 BP.
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DE cDNA encoding human PRO polypeptide #25.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1455
ID ADM12937 standard; cDNA; 3719 BP.
DE PRO4977 encoding sequence.
PN WO2004024077-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1456
ID ADM42137 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1457
ID ADM05275 standard; cDNA; 3719 BP.
DE Antipsoriatic cDNA sequence #857.
PN WO2004028479-A2.
PD 08-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1458
ID ADM27999 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 12; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1459
ID ADI95481 standard; cDNA; 3719 BP.
DE cDNA encoding human PRO polypeptide #25.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 13; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1460
ID ADI96033 standard; cDNA; 3719 BP.
DE Novel human secreted and transmembrane protein PRO4799 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 13; Length 3719;
Best Local Similarity 80.2%; Pred. No. 9.6e-46;
RESULT 1461
ID ADR07206 standard; cDNA; 3963 BP.
DE Full length human cDNA useful for treating neurological disease Seq 712.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 21.7%; Score 196.6; DB 13; Length 3963;
Best Local Similarity 80.2%; Pred. No. 9.9e-46;
RESULT 1462
ID ABA19615 standard; DNA; 4352 BP.
DE Human nervous system related polynucleotide SEQ ID NO 11946.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 5; Length 4352;
Best Local Similarity 81.4%; Pred. No. 1e-45;
RESULT 1463
ID ACN89730 standard; DNA; 4619 BP.
DE Breast cancer related marker, seq id 10880.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILENNIUM PHARM INC.
Query Match 21.7%; Score 196.6; DB 11; Length 4619;
Best Local Similarity 82.7%; Pred. No. 1e-45;
RESULT 1464
ID ABX34825 standard; cDNA; 4713 BP.
DE Human mdt cDNA SEQ ID 386.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 21.7%; Score 196.6; DB 8; Length 4713;
Best Local Similarity 72.4%; Pred. No. 1.1e-45;
RESULT 1465
ID ACN39177 standard; cDNA; 4823 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA325431, SEQ ID NO:3161.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 21.7%; Score 196.6; DB 13; Length 4823;
Best Local Similarity 72.4%; Pred. No. 1.1e-45;
RESULT 1466
ID AAK67118 standard; DNA; 5744 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21930.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 4; Length 5744;
Best Local Similarity 79.1%; Pred. No. 1.1e-45;
RESULT 1467
ID AAK66160 standard; DNA; 6153 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20972.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 4; Length 6153;
Best Local Similarity 82.6%; Pred. No. 1.2e-45;
RESULT 1468
ID AAK69113 standard; DNA; 10553 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23925.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 4; Length 10553;
Best Local Similarity 76.9%; Pred. No. 1.4e-45;
RESULT 1469
ID ABA16395 standard; DNA; 10553 BP.
DE Human nervous system related polynucleotide SEQ ID NO 8726.
PN WO200159063-A2.
PD 16-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 5; Length 10553;
Best Local Similarity 76.9%; Pred. No. 1.4e-45;
RESULT 1470
ID AAD14749 standard; DNA; 12394 BP.
DE Human glycogen synthase kinase 3 alpha genomic DNA.
PN WO200152865-A1.
PD 26-JUL-2001.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.7%; Score 196.6; DB 4; Length 12394;
Best Local Similarity 80.2%; Pred. No. 1.5e-45;
RESULT 1471
ID AAV05384 standard; DNA; 14237 BP.
DE Human cathepsin K gene.
PN WO9747642-A1.
PD 18-DEC-1997.
PA (SMIT) SMITHKLINE BEECHAM CORP.
Query Match 21.7%; Score 196.6; DB 2; Length 14237;
Best Local Similarity 81.8%; Pred. No. 1.6e-45;
RESULT 1472
ID AAU07092 standard; DNA; 14792 BP.

DE Human reproductive system related antigen DNA SEQ ID NO: 9780.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 4; Length 14792;
Best Local Similarity 75.1%; Pred. No. 1.6e-45;
RESULT 1473
ID AAV35616 standard; DNA; 15577 BP.
DE SHOX gene preliminary nucleotide sequence (HOX93).
PN WO9814568-A1.
PD 09-APR-1998.
PA (RAPP/) RAPPOLD-HOERBRAND G.
Query Match 21.7%; Score 196.6; DB 2; Length 15577;
Best Local Similarity 82.6%; Pred. No. 1.7e-45;
RESULT 1474
ID AAL07093 standard; DNA; 16851 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9781.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 4; Length 16851;
Best Local Similarity 75.1%; Pred. No. 1.7e-45;
RESULT 1475
ID AAL07094 standard; DNA; 16853 BP.
DE Human reproductive system related antigen DNA SEQ ID NO: 9782.
PN WO200155320-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 4; Length 16853;
Best Local Similarity 75.1%; Pred. No. 1.7e-45;
RESULT 1476
ID AAD58283 standard; DNA; 18099 BP.
DE Human tumour suppressor gene, lmt intron 4 DNA.
PN WO200306869-A1.
PD 14-AUG-2003.
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
Query Match 21.7%; Score 196.6; DB 9; Length 18099;
Best Local Similarity 83.1%; Pred. No. 1.8e-45;
RESULT 1477
ID ACN44570 standard; DNA; 19640 BP.
DE Human genomic sequence HCG38237.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 11; Length 19640;
Best Local Similarity 82.6%; Pred. No. 1.8e-45;
RESULT 1478
ID AAD56087 standard; DNA; 27184 BP.
DE Human FOSB carcinoma associated (CA) gene.
PN WO2003035837-A2.
PD 01-MAY-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 8; Length 27184;
Best Local Similarity 80.2%; Pred. No. 2.1e-45;
RESULT 1479
ID ADA02449 standard; DNA; 27184 BP.
DE Human FOSB carcinoma associated gene, SEQ ID NO:968.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 9; Length 27184;
Best Local Similarity 80.2%; Pred. No. 2.1e-45;
RESULT 1480
ID ADB72188 standard; DNA; 27184 BP.
DE Human FOSB gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 10; Length 27184;
Best Local Similarity 80.2%; Pred. No. 2.1e-45;
RESULT 1481
ID ADE82926 standard; DNA; 27184 BP.
DE Human FOSB genomic DNA sequence.

PN WO2003080808-A2.
PD 02-OCT-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 10; Length 27184;
Best Local Similarity 80.2%; Pred. No. 2.1e-45;
RESULT 1482
ID AAV35620 standard; DNA; 32367 BP.
DE Human SHOX (short stature homeobox containing gene) gene sequence.
PN WO9814568-A1.
PD 09-APR-1998.
PA (RAPP/) RAPPOLD-HOERBRAND G.
Query Match 21.7%; Score 196.6; DB 2; Length 32367;
Best Local Similarity 82.6%; Pred. No. 2.2e-45;
RESULT 1483
ID AAK73535 standard; DNA; 38358 BP.
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28347.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 21.7%; Score 196.6; DB 4; Length 38358;
Best Local Similarity 80.2%; Pred. No. 2.4e-45;
RESULT 1484
ID ADQ97152 standard; DNA; 58651 BP.
DE Human cancer associated sequence HD08-008, SEQ ID 128.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.7%; Score 196.6; DB 12; Length 58651;
Best Local Similarity 82.9%; Pred. No. 2.8e-45;
RESULT 1485
ID ADQ97343 standard; DNA; 61739 BP.
DE Human cancer associated sequence HD08-035, SEQ ID 320.
PN WO2004060304-A2.
PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.7%; Score 196.6; DB 12; Length 61739;
Best Local Similarity 78.1%; Pred. No. 2.8e-45;
RESULT 1486
ID AAD39317 standard; DNA; 62804 BP.
DE Human calcium/calmodulin-dependent protein kinase genomic DNA.
PN US6387677-B1.
PD 14-MAY-2002.
PA (PEKE) PE CORP NY.
Query Match 21.7%; Score 196.6; DB 6; Length 62804;
Best Local Similarity 70.6%; Pred. No. 2.9e-45;
RESULT 1487
ID ABX10916 standard; DNA; 62804 BP.
DE Genomic DNA encoding novel human kinase.
PN US2002132325-A1.
PD 19-SEP-2002.
PA (PEKE) PE CORP NY.
Query Match 21.7%; Score 196.6; DB 8; Length 62804;
Best Local Similarity 70.6%; Pred. No. 2.9e-45;
RESULT 1488
ID ADO52582 standard; DNA; 62804 BP.
DE Human kinase genomic DNA.
PN US2004101885-A1.
PD 27-MAY-2004.
PA (APPL-) APPLERA CORP.
Query Match 21.7%; Score 196.6; DB 12; Length 62804;
Best Local Similarity 70.6%; Pred. No. 2.9e-45;
RESULT 1489
ID ACN44594 standard; DNA; 74234 BP.
DE Human genomic sequence HCG15373.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 11; Length 74234;
Best Local Similarity 80.2%; Pred. No. 3.1e-45;
RESULT 1490
ID ADQ97278 standard; DNA; 86149 BP.
DE Human cancer associated sequence HD08-025, SEQ ID 254.
PN WO2004060304-A2.

PD 22-JUL-2004
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match 21.7%; Score 196.6; DB 12; Length 86149;
Best Local Similarity 82.6%; Pred. No. 3.2e-45;
RESULT 1491
ID ADP08387 standard; DNA: 94400 BP.
DE Human glycoprotein VI (platelet) (GP6;GPVI;GPVI) genomic DNA.
Query Match 21.7%; Score 196.6; DB 12; Length 94400;
Best Local Similarity 82.6%; Pred. No. 3.3e-45;
RESULT 1492
ID ADC85367 standard; DNA: 96593 BP.
DE Mouse Bln coding sequence.
PN WO2003045230-A2.
PD 05-JUN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 10; Length 96593;
Best Local Similarity 80.2%; Pred. No. 3.4e-45;
RESULT 1493
ID ADA02888 standard; DNA: 96594 BP.
DE Human BLM carcinoma associated gene, SEQ ID NO:1406.
PN WO2003057146-A2.
PD 17-JUL-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 9; Length 96594;
Best Local Similarity 80.2%; Pred. No. 3.4e-45;
RESULT 1494
ID ADB72626 standard; DNA: 96594 BP.
DE Human BLM gene.
PN WO2003008583-A2.
PD 30-JAN-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match 21.7%; Score 196.6; DB 10; Length 96594;
Best Local Similarity 80.2%; Pred. No. 3.4e-45;
RESULT 1495
ID ADM74483 standard; DNA: 96594 BP.
DE Human carcinoma associated (CA) nucleic acid #76.
PN US2004072154-A1.
PD 15-APR-2004.
PA (MORR/) MORRIS D W.
PA (ENGEL/) ENGELHARD E K.
Query Match 21.7%; Score 196.6; DB 12; Length 96594;
Best Local Similarity 80.2%; Pred. No. 3.4e-45;
RESULT 1496
ID AAD41740 standard; DNA: 99500 BP.
DE Human RECQL2 DNA #1.
PN US6399378-B1.
PD 04-JUN-2002.
PA (ISIS-) ISIS PHARM INC.
Query Match 21.7%; Score 196.6; DB 6; Length 99500;
Best Local Similarity 80.2%; Pred. No. 3.4e-45;
RESULT 1497
Query Match 21.7%; Score 196.6; DB 9; Length 110000;
Best Local Similarity 80.2%; Pred. No. 3.6e-45;
RESULT 1498
Query Match 21.7%; Score 196.6; DB 12; Length 110000;
Best Local Similarity 80.2%; Pred. No. 3.6e-45;
RESULT 1499
ID ABN9504 standard; DNA: 110096 BP.
DE Gene #1542 used to diagnose liver cancer.
PN WO200229103-A2.
PD 11-APR-2002.
PA (GENE-) GENE LOGIC INC.
Query Match 21.7%; Score 196.6; DB 6; Length 110096;
Best Local Similarity 79.1%; Pred. No. 3.6e-45;
RESULT 1500
ID ADO18808 standard; DNA: 111084 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 1627.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 21.7%; Score 196.6; DB 12; Length 111084;
Best Local Similarity 80.2%; Pred. No. 3.6e-45;

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